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22 January 2004

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Pia Høybye-Olsen

Method of modulation of interaction between receptor and ligand**Field of invention**

5 The present invention relates to a method for modulating the interaction between at least two proteins, wherein at least one of the two proteins is a functional cell-surface receptor and the other protein is the receptor ligand. The invention preferably concerns interaction of the fibroblast growth factor receptor (FGFR) and FGFR ligands. The invention further discloses a series of amino acid sequences
10 forming a binding site for FGFR in a FGFR ligand. Moreover, the present invention also discloses the methods for molecular design and screening of a candidate compound capable of modulating the interaction between FGFR and a protein having the above binding site, and provides a screening assay for identification of such a compound.

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Background of invention

Neural cell adhesion molecules (CAMs) of the immunoglobulin superfamily nucleate and maintain groups of cells at key sites during early development and in the adult.
20 In addition to their adhesive properties, CAMs homophilic and heterophilic interactions can affect intracellular signaling. Their ability to influence developmental events, including cell migration, proliferation, and differentiation may therefore result both from their adhesive as well as their signaling properties.

25 The neural cell adhesion molecule, NCAM, was the first discovered neural CAM. Since the discovery NCAM has been intensively studied and now it is well characterised.

30 NCAM belongs to the immunoglobulin (Ig) superfamily. Its extracellular part consists of five Ig-like and two fibronectin type III (F3) modules (Berezin *et al.*, 2000). NCAM assists both the cell-cell and cell-substratum interactions. NCAM binds to various extracellular matrix components such as heparin/heparan sulfate, chondroitin sulfate proteoglycans, and different types of collagen. Cell-cell interactions are mostly assisted by the NCAM homophilic interaction.

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The different modules of NCAM have been shown to perform distinct functions. Thus, NCAM homophilic binding is believed now to depend on the first three Ig modules. The heparin binding sequence is localized to the Ig2 module. NCAM also binds to the neural cell adhesion molecule L1. This interaction is believed to take place between the fourth Ig module of NCAM and an oligomannosidic moiety expressed on L1. The two membrane-proximal F3 modules of NCAM has been suggested to be involved in FGFR binding. Among a number of ligands of NCAM the most intriguing remain to be ATP. NCAM has been demonstrated to hydrolyze extracellularly adenosine triphosphate (ATP) (Dzhandzhugazyan and Bock, 1993 and 1997), and the proximal F3 modules have been suggested to be involved in this activity of NCAM. Recently, ATP has been demonstrated to be a modulator of NCAM induced neuritogenesis (Skladchikova et al., 1999). However, the role extracellular ATP, which is one of the most abundant neurotransmitters in the brain, in relation to known biological functions of NCAM is not well understood.

A number of research groups has now accumulated a large body of evidence indicating that intracellular signaling cascades underlying the NCAM-mediated axonal outgrowth are similar to signal transduction cascades which are activated due to stimulation of the fibroblast growth factor receptor (FGFR).

Fibroblast growth factor receptors (FGFRs) are a family of four closely related receptor protein tyrosine kinases consisting extracellularly of three Ig-like modules and intracellularly of a split tyrosine-kinase module (Powers *et al.*, 2000). The receptors are known as key regulators of morphogenesis, development, angiogenesis, and wound healing. FGFR activation and signaling are dependent on dimerization of the receptor which is induced by a high affinity binding of its ligand, fibroblast growth factor (FGF), and it also requires participation of cell surface heparin or heparan sulphate proteoglycans.

The major neural CAMs, NCAM, L1 and N-cadherin, all have been regarded as a new class of putative alternative ligands of FGFR, although there have not been so far obtained any evidence for a direct interaction between these CAMs and the receptor so far. The identification of a common structural motif which might be a prerequisite for the interaction with FGFR seems to be very advantageous in view of

the development of new drugs for the treatment of a variety of pathologic disorders where the regulation of activity of FGFR may play the key role.

Summary of invention

- 5 The present invention is directed to a method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site
- 10 comprises at least one of the sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising
- i) providing a compound capable of interacting with the receptor and/or the polypeptide thereby interfering with said receptor and said polypeptide interaction,
- 15 ii) adding the compound of step (i) to the at least two different proteins.

- The invention is also directed to a method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein said binding site is essentially consisting of one or more "strand-loop-strand" structural motifs, comprising
- 20 i) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with said receptor and said polypeptide interaction,
- 25 ii) adding the compound of step (i) to the at least two different proteins.

- An another aspect of the invention concerns a screening method for a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the
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sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising

- i) providing the at least two different proteins;
- ii) providing the compound;
- 5 iii) adding the compound to the at least two different proteins;
- iv) determining whether the interaction between the at least two different proteins has been modulated,
- v) selecting the compound capable of modulating the interaction between the at least two different proteins.

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Furthermore, the invention discloses an assay for sequential screening of a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the

15 at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of

- 20 i) providing the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, or a fragments or
- 25 a variants of said homologues,
- ii) adding the at least one receptor molecule of step (i) to the at least one polypeptide of step (i), or adding the at least one polypeptide of step (i) to the at least one receptor molecule of step (i) and permitting the interaction between the said receptor and said polypeptide, followed by the
- 30 iii) recording the interaction between the molecules of step (ii),
- iv) adding the candidate compound to the molecules of step (ii);
- v) recording the interaction between the molecules of step (iv), followed by the
- vi) assessment of at least one effect of the candidate compound on the interaction between the molecules of step (iv), followed by the

- vii) selection of a compound capable of modulating the interaction between the at least one functional cell-surface receptor molecule and the at least one polypeptide of step (i).

5 The method(s) and the assay of the invention are all preferably designated to the modulation of interaction between FGFR and a protein comprising the FGFR binding site, said site comprising at least one of the sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, by a compound capable of this modulation. Therefore, it is an important aspect of the invention to
10 provide a method for molecular design of such a compound, said method comprising the structural data on the binding FGFR with a protein comprising the above binding site, said data comprising a molecular model of interaction between FGFR and NCAM.

Furthermore, it is another important aspect of the invention to provide a method
15 A method for isolating a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding
20 site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146 or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of

- i) providing a method for sequential screening the candidate compound as the defined above and/or
- 25 ii) providing a method for molecular design of the candidate compound as the defined above,
- i) isolating the candidate compound.

The invention further discloses a series of peptide fragments having the sequences
30 set forth in SEQ ID NOS: 2-146, said fragments i) being involved in a direct interaction with FGFR, or being representing a part of an FGFR binding site on a FGFR ligand, and/or ii) being capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of
35 the at least two different proteins is represented by a polypeptide having a binding

site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues.

- 5 The invention also relates to a compound comprising the above peptide fragments and use of said compound for the preparation of a medicament.

Furthermore, the invention relates to

- 10 i) an antibody capable of binding to an epitope comprising a binding site for a cell surface receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragment or a variant of said antibody;
- 15 ii) an antibody capable of binding to an epitope comprising at least one of the sequences set forth in SEQ ID NOS: 1-146, or a fragment, or a variant of said antibody.

The invention also provides a method for the production of the above antibody. Furthermore, the invention also concerns the use of an antibody as the defined above for the modulation of interaction between a cell surface receptor, or a fragment or variant thereof, and a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, and for the manufacture of a medicament.

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Finally, the invention relates to a method for producing a pharmaceutical composition comprising the steps of identifying of a candidate compound and further the step of formulating the compound capable of modulating modulation of interaction between a cell surface receptor, or a fragment or variant thereof, and a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues with pharmaceutically acceptable carrier or solvent.

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Description of Drawings

Table 1 presents a summary of NOE statistics, energy terms and deviations from the idealized geometry calculated from the NMR measurements.

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Figure 1 shows the structure of the NCAM F3 module 2 and demonstrates the regions of the module involved in interaction with the FGFR1 Ig module 3 or AMP-PCP. a) Stereo view of an overlay of the backbone atoms of 30 superimposed structures. b) Ribbon representation of the structure. The N-terminal is located at the top of the picture. c and d) Changes in the chemical shifts of ^1H and ^{15}N atoms of 0.05 mM ^{15}N labeled sample of the NCAM F3 module 2 after addition of 1 mM unlabeled sample of the FGFR1 Ig module 3 (c) or 5 mM AMP-PCP (d). The chemical shifts were determined from the ^{15}N -HSQC spectra. The data are presented as averages from two independent experiments. e) Mapping of the residues of the NCAM F3 module 2 perturbed by the FGFR Ig module 3 (N⁷⁹, Q⁸¹, G⁸², K⁸³, black) onto the structure of the module. f) Mapping of the residues of the NCAM F3 module 2 perturbed by AMP-PCP, Y⁷⁴ and V⁷⁵ (black), and the residues of the ATP binding Walker motif A, A⁷⁷ENQQGKS⁸⁴ (grey) and K⁸⁵ (dark grey, outlined) to the structure of the module; all other residues are colored light grey. g) Arrangement of the complex of the NCAM F3 module 2 with ATP. K⁸³, K⁸⁵ and Y⁷⁴ are indicated on the ribbon representation of the backbone atoms.

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Figure 2 demonstrates the binding of the combined NCAM F3 modules 1 and 2 to the combined FGFR1 Ig modules 2 and 3 studied by means of surface plasmon resonance (SPR) analysis. The binding is given as a response difference (Resp. Diff.) between the binding to the sensor chip with the immobilized FGFR modules and a blank sensor chip (unspecific binding). Four independent experiments were performed using two different preparations of all proteins used.

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Figure 3 demonstrates the inhibiting effect of ATP on binding between the FGFR Ig modules 2, 3 and the NCAM F3 modules 1, 2 or the dendrimeric FG loop peptide (SEQ ID NO: 1). The binding was studied by SPR analysis. Approx. 2000 resonance units (RU) of the FGFR modules were immobilized on the sensor chip. Three independent experiments were performed. A) Binding of 30 μM F3 modules 1, 2 to the FGFR modules in the presence or absence of 10 mM ATP. B) A plot of % inhibition

by ATP of the binding between 30 μ M F3 modules 1, 2 and the immobilized FGFR modules versus the ATP concentration used for inhibition, and the calculated K_i value. C) Binding of the dendrimeric FG loop peptide (34, 17 and 8 μ M concentrations) to the immobilized FGFR modules and binding of 34 μ M peptide in the presence of 10 mM ATP.

Figure 4 demonstrates the binding between the dendrimeric EF loop peptide (SEQ ID NO: 9) and the FGFR Ig modules 2, 3 recorded by SPR. The binding is given as a response difference (Resp. Diff.) between the binding to the sensor chip with the immobilized FGFR modules and a blank sensor chip (unspecific binding). Four independent experiments were performed using two different preparations of all proteins used.

Figure 5 shows the effect of the NCAM F3 module 2 and the FG loop peptide on phosphorylation of FGFR and demonstrates the immunoprecipitation of NCAM by FGFR. A) TREX-293 cells, stably transfected with FGFR containing a C-terminal StrepII-tag, were stimulated for 20 min with either 10 ng/ml FGF2, 5 μ M F3 module 2 or 2.5 μ M dendrimeric FG loop peptide. After stimulation, FGFR was immunopurified using anti-phosphotyrosine antibodies and then analyzed by immunoblotting using antibodies against the StrepII-tag. B) HEK293 cells, transiently transfected with a His-tagged version of FGFR1, were stimulated for 20 min with either 5 μ M F3 module 2 or 25 μ M FG loop peptide. The total amount of FGFR1 and the amount of FGFR phosphorylation was estimated by immunoblotting using anti-pentahis (anti-His) and anti-phosphotyrosine (anti-pY) antibodies, respectively. Quantification of FGFR phosphorylation was performed by densitometric analysis of the band intensity. Phosphorylation was estimated relative to the control (untreated cells), which has been normalized to 1.0. Error bar represents one standard error of the mean. $P < 0.05$ by paired t-test when comparing treated cells with controls (the t-test was performed on six independent sets of non-normalized data). Ctl stands for the control, F3 – F3 module 2, FGL – FG loop peptide. C) TREX-293 cells, stably transfected with FGFR containing a C-terminal StrepII-tag, were transiently transfected with a control vector or NCAM. FGFR was purified from the cell lysate via the StrepII-tag and analyzed by immunoblotting using antibodies against NCAM.

Figure 6 shows the effect of the NCAM F3 module 2 and its FGFR binding part (the FG loop peptide (SEQ ID NO: 1)) on neurite outgrowth from hippocampal neurons.

a) Phase contrast micrograph of control (untreated) neurons. b) Phase contrast micrograph of neurons treated with 5 μ M F3 module. c) Neurite length versus the concentration of the F3 module, the FG-loop peptide and a truncated version of the peptide. d) Effect of an anti-FGFR antibody on neurite outgrowth induced by 5 μ M F3 module or 50 μ M FG loop peptide. e) Effect of substitutions of the various amino acids with Ala in the FG loop peptide or truncated versions of the peptide on neurite outgrowth from hippocampal neurons. The concentration of the various peptides was in all cases 50 μ M. Four independent experiments were performed. Error bar represents one standard error of the mean. * and ** stand for statistical significance of $p < 0.05$ and $p < 0.01$, respectively (by t-test).

Figure 7 shows the effect of the EF loop peptide (EFL-peptide) (SEQ ID NO: 9) on neurite outgrowth from hippocampal neurons. SU5402 is a specific inhibitor of FGFR1.

Figure 8 displays a sequential, structural and functional similarity between peptides derived from the FGFR binding part of NCAM and FGF2. a) Sequential alignment of the peptides, in which the signs |, |, :, · indicate the level of similarity in decreasing order from strong to low similarity; and structural alignment of the backbone atoms of the peptides from NCAM (1) and FGF2 (2). b) Effect of the FGF2 derived peptide and various Ala substituted forms on neurite outgrowth from hippocampal neurons including a comparison to the corresponding NCAM derived peptide. Four independent experiments were performed. Error bar represents one standard error of the mean. * stands for statistical significance of $p < 0.05$ (by t-test).

Figure 9 exhibits the effect of ATP (a) and AMP-PCP (b) on the potency of the NCAM F3 module 2, the monomeric FG loop peptide and a modified version of the peptide to stimulate neurite outgrowth from hippocampal neurons. Neurons were stimulated with either 5 μ M second F3 module or 50 μ M peptide in the presence of various concentrations of ATP or AMP-PCP (0, 0.4, 1.0 mM). cnt stands for control, F3 – the F3 module, FGL – the FG loop peptide, and YKK – the FG loop peptide in which Y⁷⁴, K⁸³ and K⁸⁵ were substituted with alanine. Four independent experiments

were performed. Error bar represents one standard error of the mean. * and ** stand for statistical significance of $p < 0.05$ and $p < 0.01$, respectively (by t-test).

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Detailed description of the invention**Method for modulation of interaction between two proteins**

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Cells of a multicellular organism communicate to each other and respond to a variety of signals of the cellular environment using an elaborate system of communication. This system enables a single cell to respond adequately to arrays of the signals by employing a finely tuned network of interactions between molecules of cell-surface receptors receiving the signals and the many cell-surface and intracellular proteins adapting and transmitting the signal into the cell. A minor intervention into a single interaction of this network may often lead to a major change in a specific cellular response to the extracellular signal.

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Accordingly, the present invention relates in one aspect to a method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising

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i) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with the interaction of said receptor and said polypeptide,

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ii) adding the compound of step (i) to the at least two different proteins.

Thus, modulation of interaction between a functional cell-surface receptor and another protein is the first objective of the method of the invention.

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In the present context by the term "interaction" is meant that a functional cell-surface receptor has a transient or permanent direct or indirect contact with another protein.

Functional cell surface receptor

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5 A cell-surface receptor is defined in the content of the present invention as any molecule comprising at least one polypeptide chain, said molecule being associated with the plasma membrane of a cell in such a way that enables said molecule to receive a signal at the outer side of the membrane, transduce the signal through the membrane, and convey said signal further by inducing a certain action on molecular level inside the cell, for example by inducing association or dissociation of molecular complexes, or initiating a biochemical reaction, for example auto-phosphorylation of the receptor.

10 The invention designates to a "functional cell-surface receptor". "Functional cell-surface receptor" is meant that the cell-surface receptor of the invention has an identifiable group of ligands, the binding of these ligands to the receptor induces intracellular signal transduction, which results in a physiological response of the cell. The physiological response, such as for example differentiation, proliferation, survival, apoptosis or motility of a cell, depends on the ligand that is involved in the interaction with the receptor, and/or characteristics of said interaction, such as the affinity or duration, and/or a species of the cell which expresses the receptor. By the term "ligand" is defined a compound which is capable to bind to the receptor and thereby to activate said receptor. "Activation" of a receptor is meant that after extra-
20 cellular binding of a ligand the receptor became capable to transmit the effect of "ligand binding" into a cascade of biochemical reactions collectively termed "receptor signaling" or "signal transduction" inside the cell resulting in one of the above mentioned physiological responses of the cell.

25 A capability of a cell-surface receptor to induce and/or maintain a cellular process upon the ligand binding is herein termed "biological function" of the receptor.

The functional cell-surface receptor of the invention, which recognises and interacts with another protein, is, in a preferred embodiment, a receptor of the family of fibroblast growth factor receptors (FGFRs) comprising FGFR1, FGFR2, FGFR3 and FGFR4. In the most preferred embodiment a cell-surface receptor of the invention is FGFR1 or a functional homologue thereof.

30 By the term "functional homologue of the receptor" is meant a molecule which is capable of

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- i) extracellular binding of a ligand of FGFR and thereby activating the receptor dependent signal transduction cascade in the cell, and/or
- ii) intracellular binding of an adaptor molecule of FGFR and thereby activating the receptor dependent signal transduction cascade in the cell.

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The term "binding" refers to a direct or indirect interaction between an FGFR homologue and a counter molecule having a binding site for FGFR. In the present context the counter molecule is an extracellular ligand of FGFR, or an intracellular adaptor molecule, such as for example STN, FRS, Grb, SHP2, PLC γ , PIP3. An "adaptor molecule" is defined in the content of the invention as a molecule, which is capable to recognize an "active state" of the receptor, selectively bind to such receptor and convey the signal of "activated receptor" in the cell by inducing a cascade of reactions of signal transduction.

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15 The invention relates to ligands having a relatively low affinity to FGFR. The affinity means the strength of attraction between molecules. The ligand of FGFR in the present context is determined as a molecule, which comprises at least one binding site to FGFR and is capable of low affinity binding to the receptor. Thus, according to the invention, the other protein, which is involved in interaction with the cell-surface receptor is in one aspect a ligand of FGFR.

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Binding site

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According to the invention a cell-surface receptor interacts with another protein through a receptor binding site, said binding site being located on said another protein. The binding site of a molecule may be defined as a specific part of said molecule, which is involved in interaction with another molecule. In the present context "binding site" is defined as a fragment of a protein, specific features of which confer on the protein a capacity to interact directly and selectively with another molecule, for example a receptor molecule. Under "specific features" in the present context is understood a particular amino acid sequence or the three-dimensional structure of that fragment of a protein which is referred as the binding site. By the term "selectively" in the present context is meant that the binding site is involved in interaction with the certain molecule or certain group of molecules, said molecule(s) having a specific structure which makes said molecule(s) capable to recognise the binding

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site and interact with it.

5 The present invention features a binding site to a cell-surface receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, such as the fragments, variants and homologues defined below.

10 In one aspect the binding site comprises, or at least part of which having comprising, at least one of the sequences set forth in SEQ ID NOS: 1-10, 100, 125, such as for example SEQ ID NOS: 2-10, 100, 125, or fragments or variants, or homologues said sequences, or fragments or variants of said homologues. The present invention relates to fragments having at least 40%, more preferably at least 50%, more preferably at least 60%, more preferably at least 70%, more preferably at least 80%, more
15 preferably at least 90%, more preferably at least 95% of the length of a predetermined sequence set forth in SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125, wherein an amino acid sequence homology between a fragment and the predetermined sequence is 100%. A variant in the present context is defined as an amino acid sequence having at least 60 %, more preferably at least 70%, more
20 preferably at least 80%, more preferably at least 90%, more preferably 95% homology to a sequence selected from SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125, or an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to a sequence selected from
25 SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125. A positive amino acid match is defined as an identity or similarity defined by physical and/or chemical properties of the amino acids having the same position in two compared sequences. Preferred positive amino acid matches of the present invention are K to R, E to D, L to M, Q to E, I to V, I to L, A to S, Y to W, K to Q, S to T, N to S and Q to R. The
30 homology of one amino acid sequence with another amino acid is defined as a percentage of identical amino acids in the two collated sequences. A homologue in the present context is defined as an amino acid sequence which has less than 60% homology to any of the sequences set forth in SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125 having remained some of the physical properties of the predetermined sequences, such as for example the three-dimensional structure or
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some of the functional properties, such as for example a capability to interact with another molecule, particularly with a receptor molecule. A variant of a homologue in the present context is defined as an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to a homologue of any of the sequences selected from SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125. Preferred embodiments of the positive amino acid matches is as the defined above. The invention concerns the fragments, variants and homologues, which remain a capability of the predetermined sequences to interact with the cell-surface receptor defined above.

In another embodiment the invention features a binding site comprising at least one variant, or fragment, or homologue of any of the sequences set forth in SEQ ID NOS: 1-10, 100, 125, or SEQ ID NOS: 2-10, 100, 125, said variant, or fragment, or homologue being preferably selected from the sequences identified in SEQ ID NOS: 11-99, 101-124, 126-146.

The described above binding site is characterised by specific structural features. The invention preferably features a binding site, which essentially consists of one or more "strand-loop-strand" structural motifs.

Side chains of the amino acids in a contiguous amino acid sequence interact to each other. The numerous interactions lead to folding the amino acid sequence into a specific structural pattern, such as α -helix and β -strand, which is usually determined by the amino acids of the sequence. Interactions between amino acids of the individual patterns hold the long amino acid sequence of a polypeptide folded in a compact tertiary structure. In a tertiary structure the amino acid sequence of a polypeptide tends to wind its way back and forth across the entire structure, either as an α -helix or β -strand, reversing its direction suddenly by making a turn and creating thus the loop regions. The loop regions, which may vary in length and have irregular shape, often form the binding sites for other molecules. The present invention concerns a binding site, which comprises at least one loop region. It is preferred, if the at least one loop region in the binding site connects two interacting β -strands forming thereby a "strand-loop-strand" structural motif. By the term "motif" in the present content is meant a unit of the polypeptide chain of a protein having the defined se-

quence of amino acids of certain length and/or characterised by specific structural features and/or (optionally) having certain functional capabilities common for a group of proteins.

5 Polypeptide comprising a binding site

As it has been mentioned above, certain combinations of α -helices and β -strands pack together and form a compactly folded tertiary structure of the protein. If the protein comprises a long amino acid sequence, such as for example more than 100 amino acids, its tertiary structure may consist of several modular units, each of which is called a protein domain. Domains are usually constructed from a section of polypeptide chain that contains between 50 and 350 amino acids. Because there is only a limited number of ways of combining α -helices and β -strands to make a globular structure, certain combinations of these elements may occur repeatedly in the core of related and also unrelated proteins bestowing some common structural features on these proteins. The present invention contemplates both the proteins having common structural characteristics, structurally related proteins, and structurally unrelated proteins. In a preferred embodiment the invention concerns at least two different proteins capable of interacting to each other, wherein at least one of the at least two proteins comprises at least two immunoglobulin (Ig)-like domains and/or at least two fibronectin type 3 (F3) domains, or at least one Ig-like domain and at least one F3 domain.

According to the invention a functional cell-surface receptor interacts with another protein. The invention preferably relates to the interaction between a cell-surface receptor and a heterologous protein. By the term "heterologous" in the present context is meant a protein the amino acid sequence of which has at most 40% homology and/or at most 50% of positive amino acid matches with the amino acid sequence of a polypeptide chain of the receptor. Preferably said heterologous protein is not capable itself to execute any biological function of the receptor. A heterologous protein is preferably an extracellular protein or a protein, at least part of which is exposed to the extracellular space. However, any homologous protein which has more than 40% homology and/or more than 50% of positive amino acid matches with the amino acid sequence of a polypeptide chain of the receptor is in the scope of the invention, if said protein comprises the binding site to the receptor described

above.

The present invention relates to a heterologous protein comprising the above described binding site, which is preferably selected from the group comprising trans-
5 membrane, cell-surface associated, extracellular matrix associated or soluble proteins.

A protein is in the present context defined as transmembrane if at least one part of the polypeptide chain of said protein is positioned extracellularly, at least one part of
10 the polypeptide chain of said protein is represented by the plasma membrane spanning domain, and at least one part of the polypeptide chain of said protein is positioned intracellularly, wherein the at least one extracellular part is connected with the at least one intracellular part via the at least one membrane spanning domain.

15 In the present context the plasma membrane associated protein is defined as a protein having a direct or indirect contact with the plasma membrane. The "direct" contact is meant that the protein has an immediate connection with the membrane assisted by a moiety covalently attached to said protein, such as for example a lipid moiety, for example glycosylphosphatidylinositol or a fatty acid moiety. The "indirect"
20 contact is meant that the protein has a connection with the membrane through another molecule which said protein is associated with in a complex, for example another protein, lipopolysaccharide or proteoglycan molecule.

25 The extracellular matrix associated protein in the present context is defined as a protein, or a molecule comprising a polypeptide chain, said protein or said molecule being attached to a component of the extracellular matrix through a chemical bond, or said protein or said molecule itself being an immediate component of the extracellular matrix.

30 The soluble protein in the present context is meant a protein, which is present free in solution in the extracellular space, such as for example a secreted protein, or a shed protein produced due to extracellular proteolysis of the membrane associated protein.

35 Furthermore, the invention features particular polypeptides from the above groups.

which are selected from cell adhesion molecules, cell-surface receptors, proteoglycans, membrane-anchored cell-surface proteolytic enzymes, extracellular matrix molecules, or growth factors.

- 5 Thus, in one embodiment the polypeptide of the invention is selected from the group of cell adhesion molecules comprising
- Neural Cell Adhesion Molecule (NCAM) (Swiss-Prot Ass. Nos: P13591, P13595-01, P13595),
 - Neural cell adhesion molecule L1 (Swiss-Prot Ass. Nos: Q9QYQ7, Q9QY38,
 - 10 P11627, Q05695, P32004),
 - Neural Cell Adhesion Molecule-2 (NCAM-2) (Swiss-Prot Ass. No: P36335)
 - Neuron-glia Cell Adhesion Molecule (Ng-CAM) (Swiss-Prot Ass. No: Q03696; Q90933),
 - Neural cell adhesion molecule CALL (Swiss-Prot Ass. No: O00533),
 - 15 - Neuroglian (Swiss-Prot Ass. No: P91767, P20241),
 - Nr-CAM (HBRAVO, NRCAM, NR-CAM 12) (Swiss-Prot Ass. Nos: Q92823, O15179, Q9QVN3)
 - Axonin-1/TAG-1 (Swiss-Prot Ass. Nos: Q02246, P22063, P28685),
 - Axonal-associated Cell Adhesion Molecule (AxCAM) (NCBI Ass. No: NP_031544.1; Swiss-Prot Ass. No: Q8TC35),
 - 20 - Myelin-Associated Glycoprotein (MAG) (Swiss-Prot Ass. No: P20917),
 - Neural cell adhesion molecule BIG-1 (Swiss-Prot Ass. No: Q62682),
 - Neural cell adhesion molecule BIG-2 (Swiss-Prot Ass. No: Q62845),
 - Fasciclin (FAS-2) (Swiss-Prot Ass. No: P22648),
 - 25 - Neural cell adhesion molecule HNB-3/NB-3 (Swiss-Prot Ass. Nos: Q9UQ52, P97528, Q9JMB8)
 - Neural cell adhesion molecule HNB-2/NB-2 (Swiss-Prot Ass. Nos: O94779, P07409, P97527),
 - Cadherin (Swiss-Prot Ass. No: Q9VW71),
 - 30 - Junctional Adhesion Molecule-1 (JAM-1) (Swiss-Prot Ass. Nos: Q9JKD5, O88792),
 - Neural cell adhesion F3/F11(Contactin) (Swiss-Prot Ass. Nos: Q63198, P1260, Q12860, Q28106, P14781, O93250),
 - Neurofascin (Swiss-Prot Ass. Nos: Q90924, Q91Z60; O42414),
 - 35 - B-lymphocyte cell adhesion molecule CD22 (Swiss-Prot Ass. Nos: Q9R094,

P20273),

- Neogenin (NEO1) (Swiss-Prot Ass. Nos: Q92859, P97603, Q90610, P97798),
- Intercellular Cell Adhesion Molecule-5 (ICAM-5/telencephalin) (Swiss-Prot Ass. Nos: Q8TAM9, Q60625) or
- 5 - Galactose binding lectin-12 (galectin-12) (Swiss-Prot Ass. Nos: Q91VD1, Q9JKX2, Q9NZ03),
- Galactose binding lectin-4 (galectin-4) (Swiss-Prot Ass. No: Q8K419; P38552) or fragments, or variants thereof.

10 In another embodiment the polypeptide is selected from the group of functional cell-surface receptors comprising

- Fibroblast Growth Factor Receptor 1 (FGFR1) (Swiss-Prot Ass. Nos: Q9QZM7, Q99AVV7, Q9UD50, Q63827),
- Fibroblast Growth Factor Receptor 2 (FGFR2) (Swiss-Prot Ass. Nos: Q96KM2, 15 P21802, Q63241),
- Fibroblast Growth Factor Receptor 3 (FGFR3) (Swiss-Prot Ass. Nos: Q95M13, AF487554, Q99052),
- Fibroblast Growth Factor Receptor 4 (FGFR4) (Swiss-Prot Ass. No: Q91742),
- Neurotrophin Tyrosin Kinase Type-2 (NTRKT-2) (Swiss-Prot Ass. No: 20 Q8WXJ5),
- Leukocyte Antigen Related Protein-Tyrosine Phosphatase (LAR-PTPRF) (Swiss-Prot Ass. Nos: Q9EQ17, Q64605, Q64604, Q9QW67, Q9VIS8 P10586),
- Nephlin (Swiss-Prot Ass. Nos: Q925S5, Q9JIX2, Q9ET59, Q9R044, Q9QZS7, 25 Q06500),
- Protein-Tyrosine Phosphatase Receptor type S (PTPRS) (Swiss-Prot Ass. Nos: Q64699, Q13332, O75870),
- Protein-Tyrosine Phosphatase Receptor type kappa (R-PTP-kappa) (Swiss-Prot Ass. No: Q15262),
- 30 - Protein-Tyrosine Phosphatase Receptor type D (PTPRD) (Swiss-Prot Ass. Nos: Q8WX65, Q9IAJ1, P23468, Q64487),
- Ephrin type-A receptor 8 (EPHA8/Tyrosine-Protein Kinase Receptor EEK) (Swiss-Prot Ass. Nos: O09127, P29322),
- Ephrin type-A receptor 3 (EPHA8/Tyrosine-Protein Kinase Receptor ETK- 35 1/CEK4) (Swiss-Prot Ass. No: P29318),

- Ephrin type-A receptor 2 (Swiss-Prot Ass. No: Q8N3Z2)
- Insulin Receptor (IR) (Swiss-Prot Ass. No: Q9PWN6)
- Insulin-like Growth Factor-1 Receptor (IGF-1) (Swiss-Prot Ass. Nos: Q9QVW4, P08069, P24062, Q60751, P15127, P15208)
- 5 - Insulin-related Receptor (IRR) (Swiss-Prot Ass. No: P14616),
- Tyrosine-Protein Kinase Receptor Tie-1 (Swiss-Prot Ass. Nos: 06805, P35590, Q06806),
- Roundabout receptor-1 (robo-1) (Swiss-Prot Ass. Nos: O44924, AF041082, Q9Y6N7),
- 10 - Neuronal nicotinic acetylcholine receptor alpha 3 subunit (CHRNA3) (Swiss-Prot Ass. Nos: Q8VHH6, P04757, Q8R4G9, P32297)
- Neuronal acetylcholine receptor alpha 6 subunit (Swiss-Prot Ass. Nos: Q15825, Q9R0W9)
- Platelet-Derived Growth Factor Receptor Beta (PDGFRB) (Swiss-Prot Ass. Nos: Q8R406, Q05030),
- 15 - Interleukin-6 Receptor (IL-6R) (Swiss-Prot Ass. No: Q00560),
- Interleukin-23 Receptor (IL-23R) (Swiss-Prot Ass. No: AF461422),
- Beta-common cytokine receptor of IL-3, IL5 and GmCsf (Swiss-Prot Ass. No: P32927)
- 20 - Cytokine Receptor-Like molecule 3 (CRLF1) (Swiss-Prot Ass. No: Q9JM58),
- Class I Cytokine Receptor (ZCYTOR5) (Swiss-Prot Ass. No: Q9UHH5)
- Netrin-1 receptor DCC (Swiss-Prot Ass. No: P43146),
- Leukocyte Fc Receptor-like Protein (IFGP2) (Swiss-Prot Ass. Nos: Q96PJ6, Q96KM2),
- 25 - Macrophage Scavenger Receptor 2 (MSR2) (Swiss-Prot Ass. No: Q91YK7), or
- Granulocyte Colony Stimulating Factor Receptor (G-CSF-R) (Swiss-Prot Ass. No: Q99062),
- or fragments, or variants thereof.

30 In still another embodiment the polypeptide is selected from the group of proteoglycans. More preferably the proteoglycan is selected from the group comprising heparan sulphate proteoglycans. In the most preferred embodiment the proteoglycan is perlecan (Swiss-Prot Ass. No: P98160), or a fragment, or a variant thereof.

It is also another embodiment to select the polypeptide from the group of membrane-anchored cell-surface proteolytic enzymes. Preferably the polypeptide is selected from the group comprising the pitrilysin family of metalloproteinases or the family of desintegrin and metalloproteases (ADAMs) comprising

- 5 - ADAM-8 (Swiss-Prot Ass. No: Q05910),
- ADAM-19 (Swiss-Prot Ass. Nos: Q9H013, O35674),
- ADAM-8 (Swiss-Prot Ass. No: P78325),
- ADAM-12 (Swiss-Prot Ass. Nos: O43184, Q61824),
- ADAM-28 (Swiss-Prot Ass. Nos: Q9JLN6, Q61824, Q9XSL6, Q9UKQ2),
- 10 - ADAM-33 precursor (Swiss-Prot Ass. Nos: Q8R533, Q923W9),
- ADAM-9 (Swiss-Prot Ass. Nos: Q13433, Q61072),
- ADAM-7 (Swiss-Prot Ass. Nos: Q9H2U9, O35227, Q63180),
- ADAM-1A Fertilin alpha (Swiss-Prot Ass. No: Q8R533),
- ADAM-15 (Swiss-Prot Ass. Nos: Q9QYV0, O88839, Q13444),
- 15 - Metalloproteinase-desintegrin domain containing protein (TECAM) (Swiss-Prot Ass. No: AF163291),
- Metalloproteinase 1 (Swiss-Prot Ass. Nos: O95204, Q9BSI6),
- or fragments, or variants thereof.

- 20 In yet another embodiment, the polypeptide is selected from the group of extracellular matrix molecules comprising
- Collagen type VII (Swiss-Prot Ass. No: Q63870),
 - Fibronectin (Swiss-Prot Ass. Nos: Q95KV4, Q95KV5, P07589, Q28377, U42594, O95609, P07589, P11276), or
 - 25 - Tenascin (Swiss-Prot Ass. Nos: Q15568, O00531, P10039, Q90995),
 - or fragments, or variants thereof.

- 30 In still yet another embodiment the polypeptide is selected from the group of growth factors. In the most preferred embodiment the growth factor is Cytokine-like factor-1 (CLF-1) (Swiss-Prot Ass. No: O75462), or a fragment, or a variant thereof.

- 35 In further another embodiment the polypeptide is selected from the group of soluble proteins. In the most preferred embodiment the soluble protein is SPLIT (Swiss-Prot Ass. No: Q9XYV4).

In the most preferred embodiment, the polypeptide is the neural cell adhesion molecule, NCAM, having the sequence identified in Swiss-Prot Ass. Nos: P13591, P13595-01 or P13595.

5 Affinity of interaction

Any interaction between two molecules may be characterised by its affinity, which means the strength of attraction between two molecules. The affinity of interaction is commonly expressed by a value of K_d , a dissociation equilibrium constant. K_d reflects a ratio between the rate of dissociation and the rate of binding between two molecules and thus represents a measure of the strength of binding between two molecules. The stronger the binding, the lower is the value of K_d . The invention relates to a low affinity interaction between a cell-surface receptor and another protein, such as the defined above. The low affinity interaction of the invention is characterised by K_d having a value in the range of 10^{-3} to 10^{-10} , such for example in the range of 10^{-4} to 10^{-8} .

According to the invention affinity of the interaction is determined by surface plasmon resonance analysis (SPR) or nuclear magnetic resonance spectroscopy (NMR).

20 Modulation of interaction

By the term "modulation" in relation to interaction between two molecules is meant a change in the strength of interaction, such as either a decrease or increase in the strength of interaction. Modulation of interaction takes place when it is important to adjust the strength of interaction between molecules adequately to a change in the situation dependent on said interaction. For example, modulating the strength of interaction between a receptor and receptor ligand makes possible the modulating the receptor dependent signal transduction and thereby the physiological status of the cell.

By "modulating receptor signalling" is meant activation or inhibition of the production of a cascade of messenger molecules, which normally takes place in the cell in response to activation of the receptor by the extracellular stimulus.

The receptor signaling leads to a physiological response of the cell. Therefore, modulating the strength of interaction between a receptor and the receptor ligand, otherwise termed "strength of receptor stimulation", makes possible to modulate the receptor signaling, and thereby a physiological response of the cell. It has been shown that the cellular response to stimulation of a receptor depends on the strength of receptor stimulation, which may, for example, be characterised by the value of affinity of interaction of the receptor with a ligand, and/or by the duration of such interaction. The both affinity and duration of interaction may be affected if the interacting molecules are exposed to a compound capable of modulating the interaction.

Compound

- 15 The present invention relates to a compound, which is capable of
- i) interacting with a cell-surface receptor thereby mimicking the interaction of the receptor with a ligand, and/or
 - ii) interacting with a cell-surface receptor thereby interfering with the interaction of the receptor and the receptor ligand, and/or
 - 20 iii) interacting with a cell-surface receptor ligand thereby interfering with the interaction of the receptor ligand and the receptor, and/or
 - iv) simultaneous interacting with a cell-surface receptor and the receptor ligand thereby interfering with the interaction of the receptor and the receptor ligand, and/or
 - 25 v) interacting with a molecule which is involved in assistance of the interaction between a cell-surface receptor and the receptor ligand thereby interfering with the interaction the receptor and the receptor ligand.

30 The invention in one aspect relates to compounds that are capable to interact with a site on the receptor, which is involved in interaction of the receptor with a ligand, or are capable to interact with a receptor binding site in the ligand molecule. In another aspect the invention relates to compounds that are capable to bind to another sites in the receptor or ligand presuming that such interaction will interfere with the interaction of the receptor and the ligand.

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The invention features any compounds capable of the above bindings. However, preferred compounds of the invention are selected from the group comprising peptides, carbohydrates, lipids or nucleotides. Among the preferred compounds the most preferred are peptide or nucleotide compounds.

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Accordingly, in one embodiment, the invention relates to a compound selected from the group comprising nucleotides, nucleotide analogues, nucleotide derivatives, di- or oligomers of nucleotides, or nucleotide comprising substances. Preferably a nucleotide is selected from the group comprising nucleotide triphosphates. More preferably a nucleotide triphosphate is selected from the group comprising UTP, GTP, 10 CTP, TTP and ATP or analogues, derivatives, di- or oligomers thereof, or substances comprising thereof. The most preferred nucleotide of the invention is ATP or an analogue thereof. A nucleotide analogue is defined as a molecule comprising a nucleotide base or a modified nucleotide base, a sugar residue or a modified 15 sugar residue and a mono-, di-, tri-, quadra-, or penta- ester group. It is one of preferred embodiments of the invention if a nucleotide analogue possesses an increased stability in an aquatic solution in vitro and/or an increased stability in an enzymatic system comprising an enzyme capable of utilising a nucleotide as a substrate. The content of a cell is an example of such enzymatic system. The invention 20 preferably relates to stable nucleotide triphosphate analogues, wherein at least one phosphorus group in the triphosphate ester is substituted for another chemical group, such for example CH-, S-, or NH- group.

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In another embodiment, the invention relates to a compound, which comprises a nucleotide. In a more preferred embodiment the compound comprises ATP, or an analogue thereof.

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A peptide compound of the invention may be any contiguous amino acid sequence, that meet the requirements for the compound defined above. Preferably a peptide compound comprises at least one of the sequences identified in SEQ ID NOS: 2-10, 100, 125, or a peptide fragment derived from any of the sequences set forth in SEQ ID NOS: 2-10, 100, 125. By the term "derived" in the present context is meant that the peptide compound may be represented by an amino acid sequence comprising a variant, or a fragment, or a combination of any of the sequences identified 35 in SEQ ID NOS: 2-10, 100, 125, or a combination of variants, or fragments thereof.

The present invention relates to fragments having at least 40%, more preferably at least 50%, more preferably at least 60%, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably at least 95% of the length of a predetermined sequence set forth in SEQ ID NOS: 2-10, 100, 125, wherein an amino acid sequence homology between a fragment and the predetermined sequence is 100%. A variant in the present context is defined as an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% homology to a sequence selected from SEQ ID NOS: 2-10, 100, 125, or an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to a sequence selected from SEQ ID NOS: 2-10, 100, 125. A homology of one amino acid sequence with another amino acid is defined as a percentage of identical amino acids in the two collated sequences. A positive amino acid match is defined as an identity or similarity defined by physical and/or chemical properties of the amino acids having the same position in two collated sequences. Preferred positive amino acid matches of the present invention are K to R, E to D, L to M, Q to E, I to V, I to L, A to S, Y to W, K to Q, S to T, N to S and Q to R. A combination of amino acid sequences may either be represented by a homopolymer or a heteropolymer of said sequences, wherein said homopolymer being represented a sequence comprising one or more repeats of any of the sequences selected from SEQ ID NOS: 2-10, 100, 125, and said homopolymer being represented by a sequence comprising one or more repeats of at least two different sequences selected from SEQ ID NOS: 2-10, 100, 125. A number of repeats in the sequences in a homopolymer, or a heteropolymer may be varying from 2 to 20, such as for example from 5 to 15.

Another preferred peptide compounds of the invention are those that comprise at least one of the sequences selected from SEQ ID NOS: 11-99, 101-124, 126-146, a fragment, variant or homologue thereof.

According to the invention sequences identified as SEQ ID NOS: 1-146 are derived from the sequences of FGFR receptor ligands and involved in interaction of the receptor with said ligands. Therefore, any of the sequences selected from SEQ ID NOS: 1-146 may be anticipated being capable of modulating the interaction be-

tween FGFR and FGFR ligand, said ligand comprising the binding site of the invention.

5 The amino acid sequence of the peptide compound of the invention may be of any suitable length, in that the length of the amino acid sequence is dictated by the functionality of the peptide and the formulation of the compound into a pharmaceutical composition. Thus, the compound normally comprises amino acid residues in the range of from 3-100 amino acid residues, such as from 10-90 amino acid residues, for example from 15-85 amino acid residues, such as from 20-80 amino acid residues, for example from 25-75 amino acid residues, such as from 30-70 amino acid residues, for example from 35-65 amino acid residues, such as from 40-60 amino acid residues, for example from 45-55 amino acid residues.

15 In another aspect the peptide compound comprises amino acid residues in the range of from 3 to 20 amino acid residues, such as from 3-19 amino acid residues, for example from 3-18 amino acid residues, such as from 3-17 amino acid residues, for example from 3-16 amino acid residues, such as from 3-15 amino acid residues, for example from 3-14 amino acid residues, such as from 3-13 amino acid residues.

20 In still another aspect the peptide compound encompasses a sequence of at least 6 to 16 contiguous amino acids, such as for example 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids.

25 In yet another aspect the amino acid sequence of a peptide compound as the defined above is capable of forming a strand-loop-strand fold analogous to a "strand-loop-strand" motif of the described above binding site of the invention.

30 The compound of the present invention may preferably be in the form of an oligomer (multimer) of monomers, wherein each monomer is as defined for the compound above. Particularly, multimeric peptides such as dendrimers may form conformational determinants or clusters due to the presence of multiple flexible peptide monomers. In one embodiment the compound is a dimer. In a more preferred embodiment the compound is a dendrimer, such as four peptides linked to a lysine backbone, or coupled to a polymer carrier, for example a protein carrier, such as BSA. Polymerisation such as repetitive sequences or attachment to various carriers

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are well-known in the art, e.g. lysine backbones, such as lysine dendrimers carrying 4 peptides, 8 peptides, 16 peptides, or 32 peptides. Other carriers may be lipophilic dendrimers, or micelle-like carriers formed by lipophilic derivatives, or starburst (star-like) carbon chain polymer conjugates.

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The individual monomers may be homologous, i.e. identical to one another, or the individual monomers may be heterologous, i.e. different from one another. The latter type of monomers may comprise at least two different monomers. In general dimers and multimers may comprise two or more identical monomers, or two or more monomers different from one another.

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Screening method

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It is an important aspect of the invention to provide a screening method for a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising

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- i) providing the at least two different proteins;
- ii) providing the compound;
- iii) adding the compound to the at least two different proteins;
- 25 iv) determining whether the interaction between the at least two different proteins has been modulated,
- v) selecting the compound capable of modulating the interaction between the at least two different proteins.

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30 The screening method according to invention concerns in a preferred embodiment identification of a candidate compound capable of modulating the interaction between a cell-surface receptor, wherein the receptor is FGFR, and a polypeptide, wherein the polypeptide is a FGFR ligand. More preferably FGFR is FGFR1 having the amino acid sequence identified in Swiss-Prot Seq Nos: Q9QZM7, Q99AVV7, 35 Q9UD50 or Q63827, or fragments, or variants thereof, or a functional homologue of

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said receptor. The FGFR ligand is preferably selected from the FGFR1 ligands, polypeptide chain of which comprises the described above binding site. Examples of preferred polypeptides are described above. The most preferred polypeptide for the screening method of the invention is the neural cell adhesion molecule, NCAM, having the amino acid sequence identified as Swiss-Prot Ass Nos: P13591, P13595-01 or P13595, or fragments, or variants thereof, a functional homologue thereof.

Screening assay

- 10 Modulation of a receptor-ligand interaction may be assessed by using a number of in vitro assays developed in the art. However, there are no any universal approach in selection of these assays for estimation of the capability of candidate compounds to modulate the interaction between different receptors and their ligands. The present invention provides an assay for sequential screening of a candidate compound
- 15 capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of
- 20
- 25 i) providing the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragments or a variants of said homologues,
 - 30 ii) adding the at least one receptor molecule of step (i) to the at least one polypeptide of step (i), or adding the at least one polypeptide of step (i) to the at least one receptor molecule of step (i) and permitting the interaction between said receptor and said polypeptide, followed by the
 - iii) recording the interaction between the molecules of step (ii),
 - iv) adding the candidate compound to the molecules of step (ii);
 - 35 v) recording the interaction between the molecules of step (iv), followed by the

- vi) assessment of at least one effect of the candidate compound on the interaction between the molecules of step (iv), followed by the
- vii) selection of a compound capable of modulating the interaction between the at least one functional cell-surface receptor molecule and the at least one polypeptide of step (i).

By the term "permitting the interaction" in the present content is meant that conditions of step (ii) include a suitable medium in which the interaction is favoured and long enough time interval to allow the molecules to interact.

The steps (ii)-(v) of the above assay may optionally be performed as the following: (ii) adding the compound to the at least one receptor molecule of step (i) or adding the compound to the at least one polypeptide of step (i), (iii) adding at least one polypeptide of step (i) to the compound and receptor of step (ii) or adding the at least one receptor molecule to the compound and polypeptide of step (i), (iv) recording the interaction between the molecules of step (iii). If the latter option is used, a candidate compound is selected when no interaction between the molecules of step (iii) has been recorded or the recorded interaction has been modulated compared to the interaction between said molecules in the absence of said compound. It is presumed that parameters of interaction between the receptor and the polypeptide in the absence of the compound have been assessed using any of the described below methods before performing the modified assay.

The described above assay is preferably provided by the invention for the sequential screening of a candidate compound capable of modulation of interaction between FGFR1 and the FGFR1 ligand, said ligand being one of the polypeptides described above. In a preferred embodiment the ligand is NCAM.

Assessment of the effect of a candidate compound on the interaction between the molecules for the assay may be done by using a conventional method of the art, such as for example surface plasmon resonance analysis (SPR), nucleic magnetic resonance spectroscopy (NMR), sedimentation analysis, immunoprecipitation, two-hybrid system, or resonance energy transfer (BRET or FRET). A candidate compound capable of modulating the interaction may be selected from compounds de-

creasing the strength of interaction between the receptor and the receptor ligand or from compounds increasing the strength of the interaction.

- 5 After the selection the candidate compound is according to the invention to be tested in an in vivo or in an in vitro cell system to evaluate significance of the recorded modulation for cellular metabolism. In such a system it may in one embodiment be measured a cell-surface receptor associated downstream signaling event, for example activation of a downstream protein. If the protein involved in interaction with a cell-surface receptor is represented by a receptor-like molecule, it may in another embodiment be measured a downstream signaling event associated with said protein. Therefore, the invention further provides a screening method for the compound selected on step (vii) of the above assay, comprising
- 10
- viii) adding the selected compound to at least one cell presenting the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragments or a variants of said homologues with the compound of step (vii) of the above assay,
- 15
- ix) assessing at least one effect of the compound on the cell of step (viii).
- 20

The invention preferably concerns an FGFR1-associated downstream signaling event, which may be selected from estimation of i) the FGFR1 tyrosine phosphorylation; ii) the activation of one or more intracellular proteins involved in any of the FGFR-associated signal transduction pathways, such as for example the STAT1, JNK, PLC γ , ERK, STAT5, PI3K, PKC, FRS2 and/or GRB2 proteins; and/or iii) a cell differentiation-related effect.

25

When the FGFR signalling is measured as a level of phosphorylation of FGFR, the degree of phosphorylation is estimated as at least 20% above the control value, such as at least 20-200 %, for example at least 50-200%. The control value in the present content is meant the degree of phosphorylation of FGFR in the medium where a compound capable of activation of FGFR is absent.

30

When estimating an efficient concentration of a compound with respect to modulation

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ing of the FGFR signalling, said concentration may be between 0.1-1000 μM , 1-1000 μM , for example 1-200 μM , for example 10-200 μM , such as 20-180 μM , for example 30-160 μM , such as 40-140 μM , for example 50-130 μM , such as 60-120 μM , for example 70-110 μM , such as 80-100 μM .

5 When estimating the downstream FGFR signaling effect such as a cell differentiation-related effect the invention preferably relates to cell aggregation, the formation of nodules, formation of cartilage, or two or more of said effects (Listrum, G. P. et al. J. Histochem. Cytochem. 1999, 47:1-6), such effect being detectable by light microscopy, turbidimetry, or flow cytometry. The cell differentiation-related effect may
10 also be measured as a change in expression at RNA or protein levels of bone sialoprotein (J. Bone Miner. Res. 1998, 13:1852-61; Genomics 1998, 53: 391-4), or type X collagen (Cell Tissue Res. 1998, 293: 357-64), the human ILA gene (Osteoarthritis Cartilage 1997, 5: 394-406), or type II collagen/or MGP (J Miner Res. 1997:
15 1815.23), and the like.

The FGFR tyrosine phosphorylation or activation of any of the molecules of FGFR-associated downstream signaling, such as for example STST1, JNK, PLC γ , ERK, STAT5, PI3K, PKC, FRS2 and/or GRB2 proteins, may be estimated by any conventional methods, such as for example immunocytochemistry, immunoblotting or immunoprecipitation, using commercially available antibody against the activated proteins. The degree of activation is estimated as at least 20% above/below the control value, such as at least 20-200 %, for example at least 50-200%. The control value is
20 estimated as a degree of phosphorylation of the protein of interest in the medium where a compound capable of activation of FGFR is absent.
25

In another preferred embodiment the invention concerns the downstream signaling associated with a protein involved in interaction with FGFR, said protein being the FGFR1 ligand. Such downstream signaling is understood to be associated with a
30 receptor-like ligand FGFR1. Preferred embodiments of such ligands of FGFR1 are disclosed above. It is understood that such ligands comprise the group of proteins, which have been associated with any downstream signal transduction cascade, or can potentially be associated with a downstream signal transduction cascade.

35 The most preferred a receptor-like ligand of FGFR1 of the invention is NCAM.

Therefore, the assay further concerns any in vitro or in vivo cellular systems comprising at least one cell presenting at least one molecule of functional FGFR1 or a functional homologue thereof and at least one molecule of NCAM or a functional homologue thereof.

NCAM-dependent signal transduction involves the variety of downstream molecules, activation of which upon the signaling may be measured. The invention in particular concerns the assessment of activation of focal adhesion kinase FAK, tyrosine kinase Fyn and/or cyclic-AMP response-binding element protein CREB. The degree of phosphorylation is estimated as at least 20% above/below the control value, such as at least 20-200 %, for example at least 50-200%. The control value is estimated as above.

Activation or inhibition of NCAM-dependent signal transduction may also be measured by evaluating the cellular responses on morphological level, in particular cell differentiation-related effects. Accordingly, the assay concerns in another particular embodiment evaluation of the effect of a candidate compound on NCAM-dependent cellular aggregation, cell motility, neuritogenesis, proliferation or survival.

A skilled artisan may select from a number of assays have developed in the art to evaluate the above cellular responses. Cellular aggregation and neuritogenesis may for example be evaluated as described by Skladchikova et al. J. Neurosci. Res 1999, 57: 207-18. Proliferation and apoptosis may be evaluated by using any commercially available assays and kits according to the manufacturer procedure.

It is a preferred embodiment of the invention selecting a compound capable of modulating NCAM-FGFR1 interaction by evaluating the effect of the compound on neuritogenesis. Therefore, cells of neural origin, which are capable of neuronal differentiation, are preferred by the invention. Such cell may be selected from primary cells, which have been extracted from selected areas of the neural system of an organism and maintained in culture according to standard methods, or the cells may be clonal cells, which have been transformed to immortality from different neural tumor or embryonic neural cells. Examples of such cells can be rat pheochromocytoma cells.

toma PC 12, mouse neuroblastoma N2A, human teratocarcinoma NT-2 or mouse carcinoma F9.

5 In the present invention a compound is considered promising when it is capable of doubling the neurite outgrowth of cultured cells when compared to control cells, such as improving neurite outgrowth three-fold, such as four-fold, for example five fold, such as six-fold.

10 Further, the present assay in another preferred embodiment concerns the selection of a compound, which is capable of stimulating/promoting survival of cells by modulating the FGFR1-NCAM interaction. In the present context the wording "stimulating/promoting survival" is used synonymously with the wording "preventing cell death" or "neuro-protection". By stimulating/promoting survival it is possible to prevent diseases or prevent further degeneration of the nervous system in individuals
15 suffering from a neuro-degenerative disorder. "Survival" refers to the process, wherein a cell has been traumatised and would under normal circumstances, with a high probability die, if not the compound of the invention was used to prevent said cell from degenerating, and thus promoting or stimulating survival of said traumatised cell. In particular the invention concerns promoting or stimulating the survival of
20 cell of neural origin.

A cell culture of the assay may further comprise mammalian cells of non-neural origin. Examples of such cells may for example include HEK293, COS7, CHO or TREX293. These cells may desirably be transformed to express different variants or
25 homologues of FGFR or NCAM by using the methods well known in art, such as for example methods of stable or transient transfection of cells with DNA constructs encoding different variants or homologues of FGFR and/or NCAM and/or other preferred ligands of FGFR of the invention. Such cells may be useful when using the evaluation of activation of the downstream molecules mentioned above for selection
30 of a candidate compound.

Method for molecular design of a candidate compound

35 It is a further aspect of the invention to provide a method for molecular design for a compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional

cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues comprising
5 using structural data on the binding site of NCAM with FGFR.

Based on structural data on the binding site of NCAM with FGFR the invention provides a molecular model of interaction of FGFR1 and NCAM. The structural data
10 provided by the invention disclose an amino acid sequence motif and a particular structural motif involved in the interaction these two molecules.

Accordingly, the peptide fragments

- i) encompassing a sequence of at least 6 to 16 contiguous amino acids and
- 15 ii) having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% sequence homology to the SEQ ID NO: 1 and/or
- iii) peptide fragments having the three-dimensional characteristics, such as for example strand-loop-strand fold, similar to the structural characteristics of
20 the peptide fragment corresponding to SEQ ID NO: 1, wherein the sequences homology between the aligned peptide fragments is at least 40% and/or the positive amino acid match is at least 50%.

are considered by the invention as candidate compounds capable of modulation of interaction between FGFR and NCAM. Furthermore, a peptide fragment having at
25 least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% sequence homology to any of the sequences identified in SEQ ID NOS: 2-146 is considered by the invention as a potential candidate compound and designated by the invention for the screening in the screening assay for a capability of modulation of interaction between FGFR and a
30 protein having the described above FGFR binding site.

Method for identifying a candidate compound

According to the above described methods for screening and molecular design the
35 candidate compound capable of modulating the interaction between at least two

different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues can be isolated and used for the formulation of a pharmaceutical composition.

Thus, the invention provides

10. - a method for isolating a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of
 20. i) providing a method for sequential screening the candidate compound as the defined above and/or
 - ii) providing a method for molecular design of the candidate compound as the defined above,
 - iii) isolating the candidate compound;
25. - a method for producing a pharmaceutical composition comprising the steps of identifying of a candidate compound and further the step of formulating of the compound capable of modulating the interaction between a cell surface receptor, or a fragment or variant thereof, and a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues with pharmaceutically acceptable carrier or solvent.

Peptide fragments

35

Using the described above method(s) and/or assay of the invention the peptide fragments which are capable of modulating the interaction between FGFR and a protein having the described above FGFR binding site may be identified. According the invention these peptide fragments in one embodiment are having at most about
5 100 amino acids comprising at least one of the amino acid sequences which are numbered from 2 to 146 and disclosed in the following sequence list:

NIEVWVEAENALGKKV (SEQ ID NO: 2),
ATNRQGKVKAF AHL (SEQ ID NO: 3),
RYVELYVVADSQEFQK (SEQ ID NO: 4),
10 VAENSRGKNVAKG (SEQ ID NO: 5),
GEYWCVAENQYGQR (SEQ ID NO: 6),
RLAALNGKGLGEIS (SEQ ID NO: 7),
KYIAENMKAQNVAKEI (SEQ ID NO: 8),
TIMGLKPETRYAVR (SEQ ID NO: 9),
15 KGLGEISAATEFKT (SEQ ID NO: 10),
NMGIWVQAENALG (SEQ ID NO: 11),
IWVQAENMLG (SEQ ID NO: 12),
EIWVEATNRLG (SEQ ID NO: 13),
VWVQAANALG (SEQ ID NO: 14),
20 EVWIEKDKPAKGRI (SEQ ID NO: 15),
ATNKGGEVKKNHGL (SEQ ID NO: 16),
KYVELYLVDYLEFQK (SEQ ID NO: 17),
RYVELYVVVDNAEFQ (SEQ ID NO: 18),
KYVELVIVADNREFQR (SEQ ID NO: 19),
25 KYIEYYLVLDNGEFKR (SEQ ID NO: 20),
RYLELYIVADHTLF (SEQ ID NO: 21),
KYVEMFVVVNHQRFQ (SEQ ID NO: 22),
RYVELFIVVDKERY (SEQ ID NO: 23),
KYVELFIVADDTVYRR (SEQ ID NO: 24),
30 KFIELFVVADEYVYRR (SEQ ID NO: 25),
KIVEKVIVADNSEVRK (SEQ ID NO: 26),
VELVIVADHSEAQK (SEQ ID NO: 27),
VAENSRGKNIAKG (SEQ ID NO: 28),
IAENSRGKNVARG (SEQ ID NO: 29),
35 AENSRGKNSFRG (SEQ ID NO: 30),

IASNLRGRNLAKG (SEQ ID NO: 31),
IPENSLGKTYAKG (SEQ ID NO: 32),
IAENMKAQNEAK (SEQ ID NO: 33),
QFIAENMKSHNETKEV (SEQ ID NO: 34),
5 GEYWCVAKNRVGQ (SEQ ID NO: 35),
GSYTCVAENMVGK (SEQ ID NO: 36),
GKYVCVGTNMVGER (SEQ ID NO: 37),
GNYTCVENEYG (SEQ ID NO: 38),
GEYTCLAGNSIG (SEQ ID NO: 39),
10 QYYCVAENGYG (SEQ ID NO: 40),
GEYYQAEQNGYG (SEQ ID NO: 41),
GNYTCLVENEYG (SEQ ID NO: 42),
GMYQCLAENAYG (SEQ ID NO: 43),
GMYQCAENTHG (SEQ ID NO: 44),
15 GIYYCLASNNG (SEQ ID NO: 45),
GGYYCTADNSYG (SEQ ID NO: 46),
GEYQCFARNDYG (SEQ ID NO: 47),
GEYFCLASNKMG (SEQ ID NO: 48),
GEYQCFARNKFG (SEQ ID NO: 49),
20 GEYFCLASNKMG (SEQ ID NO: 50),
GGYYCTADNNYG (SEQ ID NO: 51),
GNYSCEAENAWGTK (SEQ ID NO: 52),
GEYTCLAENSLG (SEQ ID NO: 53),
GEYECVAENGR LG (SEQ ID NO: 54),
25 GNYTCVVENKFGR (SEQ ID NO: 55),
GEYTCLAGNSIG (SEQ ID NO: 56),
GEYFCVASNPIG (SEQ ID NO: 57),
EYTCIANNQAGE (SEQ ID NO: 58),
GMYQCVAENKHLG (SEQ ID NO: 59),
30 GEYMCTASNTIGQ (SEQ ID NO: 60),
EYVCIAENKAGEQ (SEQ ID NO: 61),
GDYTLIAKNEYGK (SEQ ID NO: 62),
GFYQCVAENEAG (SEQ ID NO: 63),
GKYECVATNSAGTR (SEQ ID NO: 64),
35 GEYFCVYNNSLG (SEQ ID NO: 65),

GEYECAATNAHGR (SEQ ID NO: 66),
GAYWCQGTNSVGK (SEQ ID NO: 67),
GTYSCVAENILG (SEQ ID NO: 68),
RVAAVNGKGQGDYS (SEQ ID NO: 69),
5 RVAAINGCGIGPFS (SEQ ID NO: 70),
AVLNGKGLG (SEQ ID NO: 71),
ALNGQGLGATS (SEQ ID NO: 72),
RLAAKNRAGLGE (SEQ ID NO: 73),
RLGWTGKDLGEI (SEQ ID NO: 74),
10 TVTGLKPETSYMVK (SEQ ID NO: 75),
TLTGLKPSTRYRI (SEQ ID NO: 76),
TLTGLQPSTRYRV (SEQ ID NO: 77),
TLLGLKPDTTYDIK (SEQ ID NO: 78),
TLQGLRPETAYELR (SEQ ID NO: 79),
15 TLRGLRPETAYELR (SEQ ID NO: 80),
TLMNLRPKTGYSVR (SEQ ID NO: 81),
TVSGLKPGTRY (SEQ ID NO: 82),
TISGLKPDTTY (SEQ ID NO: 83),
TLQGLKPDYAY (SEQ ID NO: 84),
20 LRGLKPWTQYAV (SEQ ID NO: 85),
IDGLEPDTEYIVR (SEQ ID NO: 86),
LQGLKPWTQYAI (SEQ ID NO: 87),
TITGLEPGTEYTIQ (SEQ ID NO: 88),
GLKPWTQYAV (SEQ ID NO: 89),
25 TLASLKPWTQYAV (SEQ ID NO: 90),
LMGLQPATEYIV (SEQ ID NO: 91),
KGMGPMSEAVQFRT (SEQ ID NO: 92),
TLTGLKPDTTYDYK (SEQ ID NO: 93),
ISGLQPETSYSL (SEQ ID NO: 94),
30 TLLGLKPDTTYDIK (SEQ ID NO: 95),
TISGLTPETTYSI (SEQ ID NO: 96),
GNYSCLAENRLGR (SEQ ID NO: 97),
GNYTCVVENRVG (SEQ ID NO: 98),
GTYHCVATNAHG (SEQ ID NO: 99),
35 LSHNGVLTGYLLSY (SEQ ID NO: 100),

NGVLTGYVLRY (SEQ ID NO: 101),
NGVLTGYNLRY (SEQ ID NO: 102),
NGNLTGYLLQY (SEQ ID NO: 103),
VDENGVLTKYIYY (SEQ ID NO: 104),
5 THNGALVGYSVRY (SEQ ID NO: 105),
NGILTEYILKY (SEQ ID NO: 106),
NGILIGYTLRY (SEQ ID NO: 107),
THSGQITGYKIRY (SEQ ID NO: 108),
NGKITGYIYY (SEQ ID NO: 109),
10 LSHNGIFTLY (SEQ ID NO: 110),
NGILTEYTLKY (SEQ ID NO: 111),
LDPNGIITQYEISY (SEQ ID NO: 112),
NGKITGYIYY (SEQ ID NO: 113),
HLEVQAFNGRGSQPA (SEQ ID NO: 114),
15 HLTVRAYNGAGYGP (SEQ ID NO: 115),
HLSVKAYNSAGTGPS (SEQ ID NO: 116),
HLAVKAYNSAGTGPS (SEQ ID NO: 117),
NLEVRAFNSAGDGP (SEQ ID NO: 118),
HLTVLAYNSKGAGP (SEQ ID NO: 119),
20 LRVLVFNNGRGDGP (SEQ ID NO: 120),
HIDVSAFNSAGYGP (SEQ ID NO: 121),
HLAVELFNNGR (SEQ ID NO: 122),
LELQSINFLGGQPA (SEQ ID NO: 123),
HFTVRAYNGAGYGP (SEQ ID NO: 124),
25 HLEVQAFNGRGSQPA (SEQ ID NO: 125),
VIADQPTFVKYLIK (SEQ ID NO: 126),
TIKGLRPGVWYEGQ (SEQ ID NO: 127),
TLTELSPTQYTVK (SEQ ID NO: 128),
TLDDLAPDTTYLVQ (SEQ ID NO: 129),
30 TVSDVTPHAIYTVR (SEQ ID NO: 130),
IIRGLNASTRYLFR (SEQ ID NO: 131),
TLMNLRPKTGYSVR (SEQ ID NO: 132),
TLTGLKPGTEYEVN (SEQ ID NO: 133),
GPEHLMPSSTYVAR (SEQ ID NO: 134),
35 RVTGLTPKKTYEFR (SEQ ID NO: 135),

LTGLKPGTEYEFK (SEQ ID NO: 136),
EVRVQAVNGGGNGPP (SEQ ID NO: 137),
LIKVVAINDRGE (SEQ ID NO: 138),
VVSIIAVNGREE (SEQ ID NO: 139),
5 VSVYAQNQNGE (SEQ ID NO: 140),
TISLVAEKGRHK (SEQ ID NO: 141),
HLEVQAFNGRGS GPA (SEQ ID NO: 142),
HVEVQAFNGRGL GPA (SEQ ID NO: 143),
HVEVQAFNGRGL GPA (SEQ ID NO: 144),
10 EFRVRAVNGAGEG (SEQ ID NO: 145),
VARVRTRLAPGSRLS (SEQ ID NO: 146)
or a variant, or a fragment, or a homologue thereof.

15 In another embodiment, the peptide fragments are essentially consisting of at least one of the above sequences.

In still another embodiment, the peptide fragments are consisting of at least one of the above sequences.

20 The fragments, variants and homologues of the above sequences are as the defined above fragments, variants and homologues of a peptide compound.

It is an objective of the present invention to provide one or more the above amino acid sequences for the manufacture of a medicament.

25 Another objective of the invention is to use the above sequences as antigenic epitopes for the production of antibodies.

Antibodies

30 It is an objective of the present invention to provide an antibody capable of selectively binding to an epitope comprising the binding site of the invention. Therefore, any antibody capable of selectively binding to an epitope comprising

1) any of the sequences set forth in SEQ ID NOS: 1-10, 100, 125, or fragments or variants, or homologues said sequences, or fragments or variants of said
35

homologues, wherein

- 5 i) a fragment is defined as an amino acid sequence having at least 40%, more preferably at least 50%, more preferably at least 60%, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably at least 95% of the length of a predetermined sequence set forth in SEQ ID NOS: 1-10, 100, 125, wherein an amino acid sequence homology between a fragment and the predetermined sequence is 100%,
- 10 ii) a variant is defined as an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% homology to a sequence selected from SEQ ID NOS: 1-10, 100, 125 or an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to a sequence selected from SEQ ID NOS: 1-10, 100, 125, wherein a positive amino acid match is defined as an identity or similarity defined by physical and/or chemical properties of the amino acids having the same position in two compared sequences. Preferred positive amino acid matches of the present invention are K to R, E to D, L to M, Q to E, I to V, I to L, A to S, Y to W, K to Q, S to T, N to S and Q to R. The homology of one amino acid sequence with another amino acid is defined as a percentage of identical amino acids in the two collated sequences,
- 15
- 20 iii) a homologue is defined as an amino acid sequence which has less than 60% homology to any of the sequences set forth in SEQ ID NOS: 1-10, 100, 125 having remained some of the physical properties of the predetermined sequences, such as for example the three-dimensional structure or some of the functional properties, such as for example a capability to interact with another molecule, particularly with a receptor molecule,
- 25
- iv) a variant of a homologue is defined as an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to a homologue of any of the sequences selected from SEQ ID NO: 1-10, 100, 125 wherein the positive amino acid matches being as the defined above; and/or
- 30
- 2) any of the sequences identified as SEQ ID NOS: 11-99, 101-124, 126-146 or fragments or variants, or homologues said sequences, or fragments or variants of
- 35

said homologues, wherein said fragments or variants, or homologues said sequences, or fragments or variants of said homologues being defined as the above, and/or

- 5 3) a peptide fragment having structural characteristics, such as for example strand-loop-strand fold, similar to the structural characteristics of a peptide fragment corresponding to SEQ ID NO: 1, wherein the sequences homology between the aligned peptide fragments is at least 40% and/or the positive amino acid match is at least 50%
are in the scope of the invention.

10

In one embodiment the antibody is capable to modulate the cell-surface receptor function by decreasing the capability of a ligand to activate the receptor by interfering with the binding of said ligand to said receptor. In a more preferred embodiment the antibody is capable to bind to the described above epitope in a
15 FGFR ligand and thereby to modulate activating of FGFR. By "modulate" in the present context is meant to promote or inhibit the activating of the receptor. Preferred embodiments for these FGFR ligands are described above.

20

In another embodiment the antibody is capable to modulate the biological function of a cell-surface receptor ligand by interfering with the binding of said ligand to said receptor. This embodiment relates to those FGFR ligands that

- (i) may be the receptor molecules independent from FGFR, and/or
(ii) may use an alternative receptor when the FGFR signaling is inhibited, and/or
(iii) may have additional biological functions that are not associated with any
25 downstream signaling.

Preferred embodiments for such ligands comprising the epitope of the invention are described above.

30

Fragments of the polypeptides comprising the binding site of the invention can be used to raise antibodies useful in the invention. It is preferred to use for raising the above described antibodies the peptide fragments having the sequences set forth in SEQ ID NOS: 1-146, or fragments or variants, or homologues said sequences, or fragments or variants of said homologues. In general, the peptides can be coupled to a carrier protein, such as KLH, as described in Ausubel et al., *supra*, mixed with
35 an adjuvant, and injected into a host mammal. Such polypeptides or peptide frag-

ments can be produced by recombinant techniques as described the above or synthesized (see, for example, "Solid Phase Peptide Synthesis," *supra*; Ausubel et al., *supra*). Also the carrier could be PPD. Antibodies can be purified by peptide antigen affinity chromatography.

5

Thus, the invention concerns a method for the production of antibodies comprising administering to an animal a peptide fragment comprising at least one sequence selected from the sequences set forth in SEQ ID NOS: 1-146.

10

In particular, various host animals can be immunized by injection with the above peptide fragments. Host animals include rabbits, mice, guinea pigs, rats, and chickens. Various adjuvants that can be used to increase the immunological response depend on the host species and include Freund's adjuvant (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as

15

lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. Potentially useful human adjuvants include BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*. Immunizations may also be carried out by the injection of DNA encoding an FGFR-ligand or fragments thereof corresponding to the binding site. Polyclonal antibodies are heterogeneous populations of antibody molecules that are contained in the sera of the immunized animals.

20

Antibodies within the invention therefore include polyclonal antibodies and, in addition, monoclonal antibodies, humanized or chimeric antibodies, single chain antibodies, Fab' fragments, F(ab')₂ fragments, and molecules produced using a Fab expression library, and antibodies or fragments produced by phage display techniques.

25

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, can be prepared using the peptide fragments comprising the above described binding site and standard hybridoma technology (see, for example, Kohler et al., *Nature* 256:495, 1975; Kohler et al., *Eur. J. Immunol.* 6:511, 1976; Kohler et al., *Eur. J. Immunol.* 6:292, 1976; Hammerling et al., "Monoclonal Antibodies and T Cell Hybridomas," Elsevier, NY, 1981; Ausubel et al., *supra*).

30

In particular, monoclonal antibodies can be obtained by any technique that provides for the production of antibody molecules by continuous cell lines in culture such as described in Kohler et al., *Nature* 256:495, 1975, and U.S. Patent No. 4,376,110; the human B-cell hybridoma technique (Kosbor et al., *Immunology Today* 4:72, 1983; 5 Cole et al., *Proc. Natl. Acad. Sci. USA* 80:2026, 1983), and the EBV-hybridoma technique (Cole et al., "Monoclonal Antibodies and Cancer Therapy," Alan R. Liss, Inc., pp. 77-96, 1983). Such antibodies can be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. (In the case of chickens, the immunoglobulin class can also be IgY.) The hybridoma producing the mAb of this 10 invention may be cultivated *in vitro* or *in vivo*. The ability to produce high titers of mAbs *in vivo* makes this the presently preferred method of production, but in some cases, *in vitro* production will be preferred to avoid introducing cancer cells into live animals, for example, in cases where the presence of normal immunoglobulins coming from the aetis fluids are unwanted, or in cases involving ethical considerations. 15

Once produced, polyclonal, monoclonal, or phage-derived antibodies are tested for specific recognition of the above described epitope by Western blot or immunoprecipitation in samples containing the polypeptides comprising the binding site or 20 fragments thereof, e.g., as described in Ausubel et al., *supra*. Antibodies that specifically recognise and bind to a FGFR ligand are useful in the invention. For example, such antibodies can be used in an immunoassay to monitor the level of expression a FGFR ligand in a sample collected from an individual.

25 In some cases it may be desirable to minimize the potential problems of low affinity or specificity of antisera. In such circumstances, two or three fusions can be generated for each protein, and each fusion can be injected into at least two animals. Antisera can be raised by injections in a series, preferably including at least three booster injections. Spleen cells from the immunised animals may be used for generating monoclonal antibodies. 30

The antibodies can be used, for example in the detection of the FGFR ligand in a biological sample, as a part of a diagnostic assay. Antibodies can also be used in a screening assay for measuring the activity of FGFR. Thus, the antibody may be

coupled to a compound comprising a detectable marker for diagnostic purposes. The markers or labels may be selected from the described above.

5 In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., *Proc. Natl. Acad. Sci. USA*, 81:6851, 1984; Neuberger et al., *Nature*, 312:604, 1984; Takeda et al., *Nature*, 314:452, 1984) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different
10 animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent Nos. 4,946,778, 4,946,778, and 4,704,692) can be adapted to produce
15 single chain antibodies against an FGFR-ligand or a fragment thereof. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments that recognise and bind to specific epitopes can be generated
20 by known techniques. For example, such fragments include but are not limited to F(ab')₂ fragments that can be produced by pepsin digestion of the antibody molecule, and Fab' fragments that can be generated by reducing the disulfide bridges of F(ab')₂ fragments. Alternatively, Fab' expression libraries can be constructed (Huse et al., *Science*, 246:1275, 1989) to allow rapid and easy identification of monoclonal
25 Fab' fragments with the desired specificity.

Antibodies can be humanized by methods known in the art. For example, monoclonal antibodies with a desired binding specificity can be commercially humanized (Scotgene, Scotland; Oxford Molecular, Palo Alto, CA). Fully human
30 antibodies, such as those expressed in transgenic animals are also features of the invention (Green et al., *Nature Genetics* 7:13-21, 1994; see also U.S. Patents 5,545,806 and 5,569,825, both of which are hereby incorporated by reference).

35 Production of polypeptides and peptide fragments

Polypeptides and peptide fragments of the invention can be provided by any suitable conventional method known in the art. The peptide fragments and polypeptides of the invention can be for example chemically synthesized (for example, see Creighton, "Proteins: Structures and Molecular Principles," W.H. Freeman & Co., NY, 1983), or, perhaps more advantageously, produced by recombinant DNA technology as described herein. For additional guidance, skilled artisans may consult Ausubel et al. (*supra*), Sambrook et al. ("Molecular Cloning, A Laboratory Manual," Cold Spring Harbor Press, Cold Spring Harbor, NY, 1989), and, particularly for examples of chemical synthesis Gait, M.J. Ed. ("Oligonucleotide Synthesis," IRL Press, Oxford, 1984).

Recombinant molecules

The methods and the assay described above all include a step of providing at least two interacting proteins.

The two interacting proteins of the methods and the assay of the invention are preferably recombinant proteins. Therefore, the invention in additional embodiment encompasses expression vectors that contain the coding DNA sequences for the interacting proteins and genetically engineered host cells that contain any of the foregoing expression vectors and thereby express the nucleic acid molecules of the invention in the host cell.

Preferred embodiments for the expression vectors are: (a) expression vectors that contain any of the foregoing FGFRs, including FGFR1, FGFR2, FGFR3 and FGFR4, or FGFR-ligand related coding sequences, said FGFR-ligand being selected from the preferred polypeptides of the invention described above, and/or their complements (that is, "antisense" sequence); (b) expression vectors that contain any of the foregoing FGFRs or FGFR-ligand related coding sequences comprising the above mutation operatively associated with a regulatory element (examples of which are given below) that directs the expression of the coding sequences; (c) expression vectors containing, in addition to sequences encoding mutated FGFRs or FGFR-ligands, nucleic acid sequences that are unrelated to nucleic acid sequences encoding the FGFRs or FGFR-ligands, such as molecules encoding a reporter or marker.

- Recombinant nucleic acid molecule may contain a sequence encoding mutated FGFRs or FGFR-ligands, soluble FGFRs or FGFR-ligands, truncated FGFRs or FGFR-ligands, or functional domains of FGFRs, such as for example Ig 2 or Ig 3 domain of FGFR1, or the domains of a FGFR ligand, such as for example the domains of NCAM, for example the Ig-like or F3 type domains. The full-length mutated polypeptides, domains of FGFRs or FGFR-ligands, or fragments thereof may be fused to additional polypeptides, as described below.
- 10 The regulatory elements referred to above include, but are not limited to, inducible and non-inducible promoters, enhancers, operators and other elements, which are known to those skilled in the art, and which drive or otherwise regulate gene expression. Such regulatory elements include but are not limited to the cytomegalovirus hCMV immediate early gene, the early or late promoters of SV40 adenovirus, the lac system, the trp system, the TAC system, the TRC system, the major operator and promoter regions of phage A, the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase, the promoters of acid phosphatase, and the promoters of the yeast - mating factors.
- 20 Similarly, the nucleic acid can form part of a hybrid gene encoding additional polypeptide sequences, for example, sequences that function as a marker or reporter. Examples of marker or reporter genes include -lactamase, chloramphenicol acetyltransferase (CAT), adenosine deaminase (ADA), aminoglycoside phosphotransferase (neo^r, G418^r), dihydrofolate reductase (DHFR), hygromycin-B-phosphotransferase (HPH), thymidine kinase (TK), lacZ (encoding -galactosidase), green fluorescent protein (GFP), and xanthine guanine phosphoribosyltransferase (XGPRT). As with many of the standard procedures associated with the practice of the invention, skilled artisans will be aware of additional useful reagents, for example, of additional sequences that can serve the function of a marker or reporter. Generally, the hybrid
- 25 polypeptide will include a first portion and a second portion; the first portion being, for example, a portion of the FGFR1 or NCAM amino acid sequence and the second portion being, for example, the reporter described above or an immunoglobulin heavy chain.
- 30

The expression systems that may be used for purposes of the invention include, but are not limited to, microorganisms such as bacteria (for example, *E. coli* and *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA, or cosmid DNA expression vectors containing the nucleic acid molecules of the invention; yeast (for example, *Saccharomyces* and *Pichia*) transformed with recombinant yeast expression vectors containing the nucleic acid molecules encoding FGFR1 or the nucleic acid sequence encoding NCAM; insect cell systems infected with recombinant virus expression vectors (for example, baculovirus) containing the nucleic acid molecules of the invention; plant cell systems infected with recombinant virus expression vectors (for example, cauliflower mosaic virus (CaMV) and tobacco mosaic virus (TMV)) or transformed with recombinant plasmid expression vectors (for example, Ti plasmid) containing FGFR nucleotide sequences; or mammalian cell systems (for example, COS, CHO, BHK, 293, VERO, HeLa, MDCK, WI38, and NIH 3T3 cells) harbouring recombinant expression constructs containing promoters derived from the genome of mammalian cells (for example, the metallothionein promoter) or from mammalian viruses (for example, the adenovirus late promoter and the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the gene product being expressed. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther et al., *EMBO J.* 2:1791, 1983), in which the coding sequence of the insert may be ligated individually into the vector in frame with the lacZ coding region so that a fusion protein is produced; pIN vectors (Inouye and Inouye, *Nucleic Acids Res.* 13:3101-3109, 1985; Van Heeke and Schuster, *J. Biol. Chem.* 264:5503-5509, 1989); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhydrosis virus (AcNPV) can be used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The coding sequence of the insert may be cloned individually into

non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of the coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (for example, see Smith et al., *J. Virol.* 46:584, 1983; Smith, U.S. Patent No. 4,215,051).

10 In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the nucleic acid molecule of the invention may be ligated to an adenovirus transcription/translation control complex, for example, the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (for example, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a FGFR gene product in infected hosts (for example, see Logan and Shenk, *Proc. Natl. Acad. Sci. USA* 81:3655-3659, 1984). Specific initiation signals may also be required for efficient translation of inserted nucleic acid molecules. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire gene or cDNA, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the coding sequence is inserted, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., *Methods in Enzymol.* 153:516- 544, 1987).

In addition, a host cell strain may be chosen, which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (for example, glycosylation) and processing (for

example, cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. The mammalian cell types listed above are among those that could serve as suitable host cells.

10

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines, which stably express the FGFR sequences or any FGFR ligand sequences described above may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (for example, promoter, enhancer sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. Such engineered cell lines may be particularly useful in the screening assay and evaluation of candidate compounds that affect the interaction between FGFR and an FGFR ligand.

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A number of selection systems can be used. For example, the herpes simplex virus thymidine kinase (Wigler, et al., *Cell* 11:223, 1977), hypoxanthine- guanine phosphoribosyltransferase (Szybalska and Szybalski, *Proc. Natl. Acad. Sci. USA* 48:2026, 1962), and adenine phosphoribosyltransferase (Lowy, et al., *Cell* 22:817, 1980) genes can be employed in *tk⁻*, *hgprt⁻* or *aprt⁻* cells, respectively. Also, anti-metabolite resistance can be used as the basis of selection for the following genes: *dhfr*, which confers resistance to methotrexate (Wigler et al., *Proc. Natl. Acad. Sci. USA* 77:3567, 1980; O'Hare et al., *Proc. Natl. Acad. Sci. USA* 78:1527, 1981); *gpt*, which confers resistance to mycophenolic acid (Mulligan and Berg, *Proc. Natl. Acad. Sci. USA* 78:2072, 1981); *neo*, which confers resistance to the aminoglycoside G-

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418 (Colberre-Garapin et al., *J. Mol. Biol.* 150:1, 1981); and hygromycin, which confers resistance to hygromycin (Santerre et al., *Gene* 30:147, 1984).

5 Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (*Proc. Natl. Acad. Sci. USA* 88: 8972-8976, 1991). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-
10 terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni^{2+} -nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

15 It is presumed that molecules of one group of the recombinant proteins of the invention comprise the described above binding site, and molecules of another group of the recombinant proteins comprise a site for recognition of said binding site.

Medicament

20 Activation of cell-surface receptors upon the ligand binding is strictly regulated in a healthy organism. Mutations, abnormal expression or processing of a receptor or the receptor ligands lead to abnormalities in activity of the receptor and therefore lead to dysfunction of the receptor. The dysfunction of the receptor is in turn a reason for
25 dysfunction of the cells which use the receptor for maintenance of various cellular processes. The latter is a manifestation of a disease. FGFRs are expressed by a wide variety of cell species during embryonic development and in the adult. Dysfunction of these receptors has been associated with a number of diseases.

30 Accordingly, it is an objective of the invention to provide a compound capable of modulation of the activity of FGFRs, said compound being concerned by the invention as a medicament for the treatment of diseases, wherein modulation of the activity of FGFRs may be considered as an essential condition for the curing.

35 Thus, the medicament of the invention is in one embodiment for the treatment of
1) normal, degenerated or damaged NCAM presenting cells, and/or

- 2) diseases and conditions of the central and peripheral nervous system, or of the muscles or of various organs, and/or
- 3) diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic damage, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression; for treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as after organ transplantation, or such as genetic or traumatic atrophic muscle disorders; or for treatment of diseases or conditions of various organs, such as degenerative conditions of the gonads, of the pancreas such as diabetes mellitus type I and II, of the kidney such as nephrosis and of the heart, liver and bowel, and/or
- 4) postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression, and/or
- 5) cancer disease, wherein the cancer is any type of solid tumors requiring neoangiogenesis.
- In another embodiment the medicament of the invention is for the manufacture of a medicament for
- 1) promotion of wound-healing, and/or
 - 2) prevention of cell death of heart muscle cells, such as after acute myocardial infarction, or after angiogenesis, and/or
 - 3) revascularisation, and/or
 - 4) stimulation of the ability to learn and/or of the short and/or long-term memory.

In one embodiment the medicament of the invention comprises at least one the amino acid sequences set forth in SEQ ID NOS: 2-146, or fragments or variants, or homologues said sequences, or fragments or variants of said homologues. In

another embodiment the medicament of the invention comprises an antibody capable of binding to an epitope comprising the binding site of the invention, or a fragment, or a variant of said antibody.

5 The medicament of the invention comprises an effective amount of one or more of the compounds as defined above, or a composition as defined above in combination with pharmaceutically acceptable additives. Such medicament may suitably be formulated for oral, percutaneous, intramuscular, intravenous, intracranial, intrathecal, intracerebroventricular, intranasal or pulmonal administration.

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Strategies in formulation development of medicaments and compositions based on the compounds of the present invention generally correspond to formulation strategies for any other protein-based drug product. Potential problems and the guidance required to overcome these problems are dealt with in several textbooks, e.g.

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"Therapeutic Peptides and Protein Formulation. Processing and Delivery Systems", Ed. A.K. Banga, Technomic Publishing AG, Basel, 1995.

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Injectables are usually prepared either as liquid solutions or suspensions, solid forms suitable for solution in, or suspension in, liquid prior to injection. The preparation may also be emulsified. The active ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol or the like, and combinations thereof. In addition, if desired, the preparation may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or which enhance the effectiveness or transportation of the preparation.

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Formulations of the compounds of the invention can be prepared by techniques known to the person skilled in the art. The formulations may contain pharmaceutically acceptable carriers and excipients including microspheres, liposomes, microcapsules, nanoparticles or the like.

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The preparation may suitably be administered by injection, optionally at the site, where the active ingredient is to exert its effect. Additional formulations which are suitable for other modes of administration include suppositories, nasal, pulmonal

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and, in some cases, oral formulations. For suppositories, traditional binders and carriers include polyalkylene glycols or triglycerides. Such suppositories may be formed from mixtures containing the active ingredient(s) in the range of from 0.5% to 10%, preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and generally contain 10-95% of the active ingredient(s), preferably 25-70%.

Other formulations are such suitable for nasal and pulmonal administration, e.g. inhalators and aerosols.

The active compound may be formulated as neutral or salt forms. Pharmaceutically acceptable salts include acid addition salts (formed with the free amino groups of the peptide compound) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic acid, oxalic acid, tartaric acid, mandelic acid, and the like. Salts formed with the free carboxyl group may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The preparations are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective. The quantity to be administered depends on the subject to be treated, including, e.g. the weight and age of the subject, the disease to be treated and the stage of disease. Suitable dosage ranges are per kilo body weight normally of the order of several hundred μg active ingredient per administration with a preferred range of from about 0.1 μg to 5000 μg per kilo body weight. Using monomeric forms of the compounds, the suitable dosages are often in the range of from 0.1 μg to 5000 μg per kilo body weight, such as in the range of from about 0.1 μg to 3000 μg per kilo body weight, and especially in the range of from about 0.1 μg to 1000 μg per kilo body weight. Using multimeric forms of the compounds, the suitable dosages are often in the range of from 0.1 μg to 1000 μg per kilo body weight, such as in the range of from about 0.1 μg to 750 μg per kilo body weight, and especially in the range of from about 0.1 μg to 500 μg per

kilo body weight such as in the range of from about 0.1 µg to 250 µg per kilo body weight. In particular when administering nasally smaller dosages are used than when administering by other routes. Administration may be performed once or may be followed by subsequent administrations. The dosage will also depend on the route of administration and will vary with the age and weight of the subject to be treated. A preferred dosage of multimeric forms would be in the interval 1 mg to 70 mg per 70 kg body weight.

For most indications a localised or substantially localised application is preferred.

Some of the compounds of the present invention are sufficiently active, but for some of the others, the effect will be enhanced if the preparation further comprises pharmaceutically acceptable additives and/or carriers. Such additives and carriers will be known in the art. In some cases, it will be advantageous to include a compound, which promote delivery of the active substance to its target.

In many instances, it will be necessary to administrate the formulation multiple times. Administration may be a continuous infusion, such as intraventricular infusion or administration in more doses such as more times a day, daily, more times a week, weekly, etc. It is preferred that administration of the medicament is initiated before or shortly after the individual has been subjected to the factor(s) that may lead to cell death. Preferably the medicament is administered within 8 hours from the factor onset, such as within 5 hours from the factor onset. Many of the compounds exhibit a long term effect whereby administration of the compounds may be conducted with long intervals, such as 1 week or 2 weeks.

In connection with the use in nerve guides, the administration may be continuous or in small portions based upon controlled release of the active compound(s). Furthermore, precursors may be used to control the rate of release and/or site of release. Other kinds of implants and well as oral administration may similarly be based upon controlled release and/or the use of precursors.

Treatment

Treatment by the use of the compounds/compositions according to the invention is

In one embodiment useful for inducing differentiation, modulating proliferation, stimulate regeneration, neuronal plasticity and survival of cells being implanted or transplanted. This is particularly useful when using compounds having a long term effect.

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In further embodiment the treatment may be for stimulation of survival of cells which are at risk of dying due to a variety of factors, such as traumas and injuries, acute diseases, chronic diseases and/or disorders, in particular degenerative diseases normally leading to cell death, other external factors, such as medical and/or surgical treatments and/or diagnostic methods that may cause formation of free radicals or otherwise have cytotoxic effects, such as X-rays and chemotherapy. In relation to chemotherapy the FGFR binding compounds according to the invention are useful in cancer treatment of all cancer cells presenting FGFRs.

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Thus, the treatment comprises treatment and/or prophylaxis of cell death in relation to diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, e.g. resulting from spinal cord injury, impaired myelination of nerve fibers, postischaemic damage, e.g. resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve degeneration associated with diabetes mellitus, neuro-muscular degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease, or Huntington's disease.

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Also, in relation to diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as genetic or traumatic atrophic muscle disorders; or for the treatment of diseases or conditions of various organs, such as degenerative conditions of the gonads, of the pancreas, such as diabetes mellitus type I and II, of the kidney, such as nephrosis the compounds according to the invention may be used for inducing differentiation, modulating proliferation, stimulate regeneration, neuronal plasticity and survival, i.e. stimulating survival.

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Furthermore, the compound and/or pharmaceutical composition may be for preventing cell death of heart muscle cells, such as after acute myocardial infarction, in order to induce angiogenesis. Furthermore, in one embodiment the compound and/or pharmaceutical composition is for the stimulation of the survival of heart

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muscle cells, such as survival after acute myocardial infarction. In another aspect the compound and/or pharmaceutical composition is for revascularisation, such as after injuries.

5 It is also within the scope of the invention to use the compound and/or pharmaceutical composition for the promotion of wound-healing. The present compounds are capable of stimulating angiogenesis and thereby promote the wound healing process.

10 The invention further discloses the use of the compound and/or pharmaceutical composition in the treatment of cancer. Regulation of activation of FGFR is important for tumor agiogenesis, proliferation and spreading.

In yet a further embodiment the use of the compound and/or pharmaceutical composition is for the stimulation of the ability to learn and/or of the short and/or long term memory, as FGFR activity is important for differentiation of neural cells.

In particular the compound and/or pharmaceutical composition of the invention may be used in the treatment of clinical conditions, such as Neoplasms such as malignant neoplasms, benign neoplasms, carcinoma in situ and neoplasms of uncertain behavior, diseases of endocrine glands, such as diabetes mellitus, psychoses, such as senile and presenile organic psychotic conditions, alcoholic psychoses, drug psychoses, transient organic psychotic conditions, Alzheimer's disease, cerebral lipidoses, epilepsy, general paresis [syphilis], hepatolenticular degeneration, Huntington's chorea, Jakob-Creutzfeldt disease, multiple sclerosis, Pick's disease of the brain, syphilis, Schizophrenic disorders, affective psychoses, neurotic disorders, personality disorders, including character neurosis, nonpsychotic personality disorder associated with organic brain syndromes, paranoid personality disorder, fanatic personality, paranoid personality (disorder), paranoid traits, sexual deviations and disorders, mental retardation, disease in the nervous system and sense organs, cognitive anomalies, inflammatory disease of the central nervous system, such as meningitis, encephalitis, Cerebral degenerations such as Alzheimer's disease, Pick's disease, senile degeneration of brain, communicating hydrocephalus, obstructive hydrocephalus, Parkinson's disease including other extra pyramidal disease and abnormal movement disorders, spinocerebellar disease, cerebellar ataxia,

Marie's, Sanger-Brown, Dyssynergia cerebellaris myoclonica, primary cerebellar degeneration, such as spinal muscular atrophy, familial, juvenile, adult spinal muscular atrophy, motor neuron disease, amyotrophic lateral sclerosis, motor neuron disease, progressive bulbar palsy, pseudobulbar palsy, primary lateral sclerosis, other anterior horn cell diseases, anterior horn cell disease, unspecified, other diseases of spinal cord, syringomyelia and syringobulbia, vascular myelopathies, acute infarction of spinal cord (embolic) (nonembolic), arterial thrombosis of spinal cord, edema of spinal cord, subacute necrotic myelopathy, subacute combined degeneration of spinal cord in diseases classified elsewhere, myelopathy, drug-induced, radiation-induced myelitis, disorders of the autonomic nervous system, disorders of peripheral autonomic, sympathetic, parasympathetic, or vegetative system, familial dysautonomia [Riley-Day syndrome], idiopathic peripheral autonomic neuropathy, carotid sinus syncope or syndrome, cervical sympathetic dystrophy or paralysis. peripheral autonomic neuropathy in disorders classified elsewhere, amyloidosis, diseases of the peripheral nerve system, brachial plexus lesions, cervical rib syndrome, costoclavicular syndrome, scalenus anterior syndrome, thoracic outlet syndrome, brachial neuritis or radiculitis, including in newborn. Inflammatory and toxic neuropathy, including acute infective polyneuritis, Guillain-Barre syndrome, Postinfectious polyneuritis, polyneuropathy in collagen vascular disease, disorders affecting multiple structures of eye, purulent endophthalmitis, diseases of the ear and mastoid process, chronic rheumatic heart disease, ischaemic heart disease, arrhythmia, diseases in the pulmonary system, abnormality of organs and soft tissues in newborn, including in the nerve system, complications of the administration of anesthetic or other sedation in labor and delivery, diseases in the skin including infection, insufficient circulation problem, injuries, including after surgery, crushing injury, burns. Injuries to nerves and spinal cord, including division of nerve, lesion in continuity (with or without open wound), traumatic neuroma (with or without open wound), traumatic transient paralysis (with or without open wound), accidental puncture or laceration during medical procedure, injury to optic nerve and pathways, optic nerve injury, second cranial nerve, injury to optic chiasm, injury to optic pathways, injury to visual cortex, unspecified blindness, injury to other cranial nerve(s), injury to other and unspecified nerves. Poisoning by drugs, medicinal and biological substances, genetic or traumatic atrophic muscle disorders; or for the treatment of diseases or conditions of various organs, such as degenerative conditions of the gonads, of the pancreas, such as diabetes mellitus type I and II, of the kidney, such as nephrosis.

A further aspect of the invention is a process of producing a pharmaceutical composition, comprising mixing an effective amount of one or more of the compounds of the invention, or a pharmaceutical composition according to the invention with one
5 or more pharmaceutically acceptable additives or carriers, and administer an effective amount of at least one of said compound, or said pharmaceutical composition to a subject.

In one embodiment of the process as mentioned above, the compounds are used in
10 combination with a prosthetic device, wherein the device is a prosthetic nerve guide. Thus, in a further aspect, the present invention relates to a prosthetic nerve guide, characterised in that it comprises one or more of the compounds or the pharmaceutical composition as defined above. Nerve guides are known in the art.

15 The invention relates to the use a pharmaceutical composition comprising the compound of invention for the treatment or prophylaxis of any of the diseases and conditions mentioned above.

In yet a further aspect the invention relates to a method of treating a disease or condition as discussed above by administering a compound as defined herein.
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Examples

Production of recombinant proteins

25 The NCAM F3 modules 1, 2 (without expression of exons a, AAG), and FGFR1 Ig modules 2, 3 were produced using rat NCAM cDNA and mouse FGFR1 (IIIC isoform) cDNA. The F3 module 1 and the combined F3 modules 1, 2 consist of AGHHHHHH and amino acids 507-611 and 507-705 of NCAM (swissprot p13596),
30 respectively. The F3 module 2 consists of AG and amino acids 612-705 of NCAM (swissprot p13596), and is sequentially numbered from 1 to 96, A being numbered 1. The FGFR Ig module 2 consists of AGHHHHHH and amino acids 140-251 of FGFR (swissprot p16092). The FGFR Ig module 3 and the combined Ig modules 2, 3 consist of RSHHHHHH and amino acids 249-365 and 141-365 of FGFR (swissprot
35 p16092), respectively. The F3 modules and the FGFR Ig module 2 were expressed

in a KM71 strain of yeast *P. pastoris* (Invitrogen, USA) as described (Thomsen et al., 1996). The FGFR Ig module 3 and modules 2, 3 were expressed in *Drosophila* S2 cells (Invitrogen, USA) according to the manufacturer's instructions. All the proteins were purified by affinity chromatography using Ni²⁺-NTA resin (Qiagen, USA) and/or ion exchange chromatography and gel filtration. ¹⁵N-labelled F3 module 2 was produced as described (Thomsen et al., 1996). The NCAM Ig modules 1, 2 and 3 (RV and amino acids 20-308 of rat NCAM, swissprot p13596) was produced as described (Soroka et al., 2002).

10 NMR analysis: the structure calculations of the NCAM F3 module 2 and identification of the residues involved in binding with FGFR and ATP

The following samples were used for the structure determination of the NCAM F3 module 2: 2 mM module in H₂O or D₂O and 1 mM ¹⁵N-labelled module in H₂O. The buffer was 30 mM NaCl, 10 mM sodium phosphate buffer, pH 7.27. The following NMR spectra were recorded and used for assignment: TOCSY in H₂O or D₂O (45 and 70 ms mixing time), NOESY in H₂O or D₂O (80 and 200 ms mixing time), DQFCOSY, ¹⁵N-HSQC, ¹⁵N-TOCSY-HSQC (70 ms mixing time), and ¹⁵N-NOESY-HSQC (125 ms mixing time) (Bodenhausen and Ruben, 1980; Braunschweiler and Ernst, 1983; Kumar et al., 1981; Piantini et al., 1982; Zhang et al., 1994). The NMR experiments were performed on a Bruker AMX-600 MHz and Varian Unity Inova 500, 750 and 800 MHz spectrometers. All spectra were recorded at 298 K. The assignment of the ¹H and ¹⁵N resonances were performed using the program PRONTO (Kjær et al., 1994).

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Structure calculation

A distance geometry/simulated annealing protocol using the X-PLOR program was used for structure calculation. The NOE restraints were derived from 80/200 ms NOESY and 125ms ¹⁵N-NOESY-HSQC spectra with upper bounds of 2.7, 3.3 and 6.0 Å increased by 0.5 Å if the restraint included a methyl group. 40 ϕ angles restraints with bounds of -120±40° and -57±40° (derived from the ³J_{HNHα} coupling constants) and 4 χ¹ angles were applied. After inspection of hydrogen bond energies, 80 hydrogen bond restraints were applied as NOE restraints with upper bounds of 2 Å and 3 Å for the NH-O and N-O distances, respectively. Of 96 structures calcu-

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lated, 96 were accepted by X-PLOR, discriminating any structure with an NOE restraint violation $>0.5\text{\AA}$ or an angle violation $>5^\circ$. The structures were examined with MOLMOL, PROCHECK_NMR and WHATCHECK programs. 78 structures had the absolute values of the Z-scores for the 2nd generation packing quality, the Ramachandran plot, the χ_1/χ_2 plot and the backbone conformation less than 3.0. From these 78 structures, 30 structures with the absolute values of the Z-scores less than 2.4 were chosen to represent the structure of the F3 module 2.

Determination of the structure of the NCAM F3 module 2 by NMR

An overlay of 30 superimposed structures for the backbone atoms is shown in Fig. 1A (accession number 1LWR, Protein Data Bank). A ribbon representation of the structure labeling the 7 β -strands is shown in Fig. 1B. A summary of the structural statistics is given in Table 1.

The structure consists of 7 antiparallel β -strands arranged in a sandwich of two β sheets, one containing three strands (ABE) and the other four strands (GFCD). Both of the β sheets have a right-handed twist. The triple-stranded β sheet consists of residues K⁷ – G¹³ (A), S¹⁸ – I²⁴ (B), H⁵⁹ – S⁶³ (E), and the four-stranded β sheet consists of residues I³³ – A⁴² (C), I⁵¹, A⁵² (D), E⁷⁰ – N⁷⁹ (F) and G⁸² – R⁹² (G). There are two wide type β -bulges (Chan *et al.*, 1993) involving residues K⁶⁵, A⁶⁸ and V⁷⁸ (G and F β -strands), and residues A⁷⁷ and H³⁵, Y³⁶ (F and C β -strands). The two β -bulges contribute to the right-handed twist conformation of the four-stranded β -sheet. Analysis of the characteristic β -sheet inter-strand NOEs shows unambiguously that this module has the fibronectin type III fold.

Identification of the residues of the NCAM F3 module 2 interacting with FGFR and ATP

In the ¹⁵N-HSQC spectrum of an ¹⁵N-labeled protein, a signal for each amino acid with both a nitrogen and proton can be observed. The changes in the chemical shifts of the signals provide a method for the identification of residues in a protein that are perturbed by the binding of another molecule. To a 50 μM ¹⁵N-labeled sample of the NCAM F3 module 2, 1 mM unlabeled FGFR Ig modules 2 or 3, or 5 mM AMP-PCP (a non-hydrolysable analogue of ATP) were added. No significant changes of the

chemical shifts were found in the presence of the Ig module 2 (data not shown). The recorded changes of the chemical shifts in the presence of the Ig module 3 or AMP-PCP are shown in Fig. 1C,D. The residues of the F3 module that exhibited perturbation by the Ig module 3 were N⁷⁹, Q⁸¹, G⁸² and K⁸³ (Fig. 1C). The changes of the chemical shifts of these residues demonstrate that the presence of the Ig module 3 close to the F3 module 2 alters the chemical environment at the perturbed residues of the F3 module, indicating that the perturbed residues are either a part or in the vicinity of the binding site for the interaction between the two modules. These residues are located in the turn region between the F and G β -strands, and as can be seen from Fig. 2E, they are close to the N-terminus of the module and, thus, close to the C-terminus of the F3 module 1 in the NCAM molecule. Since the recombinant protein consisting of the combined F3 modules 1, 2 was found to bind to FGFR with a much higher affinity than any of the two individual F3 modules, it is possible that the perturbed residues at the N-terminus of the F3 module 2 together with residues at the C-terminus of the F3 module 1 form a single binding site which is destroyed when the F3 modules are separated, thus greatly reducing their affinity to FGFR compared to the double module protein.

The residues of the F3 module perturbed by AMP-PCP were Y⁷⁴ and V⁷⁵. The side chain of Y⁷⁴ is exposed on the surface of the module and located in the close vicinity of the nucleotide binding motif: A⁷⁷ENQQGKS⁸⁴ and K⁸⁵ (Fig. 1E). Both K⁸³ and K⁸⁵ are exposed on the surface of the module, and presumably the positively charged side chains of K⁸³ and K⁸⁵ interact with the negatively charged triphosphate moiety of ATP, whereas the side chain of Y⁷⁴ is involved in a hydrophobic interaction with the adenosine moiety of ATP. A possible arrangement of the complex of ATP and the F3 module 2 is depicted in Fig. 1G. The residues perturbed by the FGFR Ig module 3 (N⁷⁹, Q⁸¹, G⁸² and K⁸³) are also a part of the nucleotide binding motif, indicating that the ATP binding site and the FGFR binding site are overlapping.

Thus, these data indicate that N⁷⁹, Q⁸¹, G⁸² and K⁸³ of the NCAM F3 module 2 are located in a site binding to FGFR, and that the FGFR binding site overlaps the ATP binding site.

SPR Analysis of interaction between FGFR and NCAM

Binding analysis was performed using a BIAcoreX instrument (Biosensor AB) at 25 °C using 10 mM sodium phosphate pH 7.4, 150 mM NaCl as running buffer. The flow-rate was 5 µl/min. Data were analysed by non-linear curve-fitting using the manufacture's software. The FGFR Ig modules 2, 3 were immobilized on a sensor chip CM5 using amine coupling kit (Biosensor AB) as follows: 1) the two halves of the chip (designated Fc1 and Fc2) were activated by 20 µl activation solution; 2) the protein was immobilized on Fc1 using 12 µl 20 µg/ml protein in 10 mM sodium phosphate buffer pH 6.0; 3) Fc1 and Fc2 were blocked by 35 µl blocking solution. Binding of various compounds to the immobilized FGFR modules was studied as follows: A compound was injected simultaneously into Fc1 (with the immobilized FGFR modules) and Fc2 (with nothing immobilized). The curve representing unspecific binding of the compound to the surface of Fc2 was subtracted from the curve representing binding of the protein to the immobilized FGFR modules and the surface of Fc1. The resulting curve was used for analysis. For ATP competition experiments, the specified compounds were preincubated for 10 min with ATP at a specified concentration. The K_i of ATP for the interaction between the NCAM F3 modules 1, 2 and the FGFR modules 2, 3 was estimated as previously described (Kiselyov et al, 1997): The initial binding rates of 30 µM F3 modules, V_0 , and 30 µM F3 modules preincubated with ATP at a specified concentration, V_{ATP} , were determined. The % inhibition, $I\%$, was calculated using the formula: $I\% = (1 - V_{ATP}/V_0) \times 100$. $I\%$ was plotted against ATP concentration and K_i was calculated by non-linear fitting of the theoretical curve to the experimental data.

Demonstration of a direct interaction between NCAM and FGFR

From Fig. 2 it appears that a protein consisting of the NCAM F3 modules 1, 2 binds to an immobilized protein comprising the FGFR modules 2, 3, whereas a control protein consisting of the NCAM Ig modules 1, 2 and 3 does not bind to the FGFR fragment. The dissociation constant (K_d) and the coefficients of association and dissociation were: 9.97 ± 0.37 µM, 889 ± 332 M⁻¹s⁻¹ and $5.56 \pm 0.07 \times 10^{-3}$ s⁻¹ (mean ± standard deviation), respectively.

Thus, these data show that the NCAM F3 modules bind directly to FGFR

Binding of NCAM to FGFR can be inhibited by ATP

As the NCAM sites binding to FGFR and ATP overlap, then ATP might be expected to interfere with the NCAM-FGFR binding. To test this assumption, SPR analysis was used. As can be seen from Fig. 3A, adding 10 mM ATP to 30 μ M NCAM F3 modules 1, 2 completely inhibited binding of the F3 modules to the FGFR Ig modules 2, 3. To determine the inhibition constant (K_i), the inhibition effect was measured at various ATP concentrations (Fig. 3B). The calculated K_i was 0.37 ± 0.05 mM. Since the NMR experiments indicate that the turn region between the F and G β -strands of the F3 module 2 is involved in binding to FGFR, it was of interest to test if a peptide fragment spanning these residues could bind to FGFR. Moreover, another peptide fragment located in the F3 module 1 was of interest to test, as the turn region between the E and F strands of this module may constitute an N-terminal part of the binding site in NCAM interacting with the Ig2-Ig3 module of FGFR. For this purpose, a peptide corresponding to residues E⁷² – A⁸⁵ of the F3 module 2 (SEQ ID NO: 1) (termed the FG loop peptide) and a peptide corresponding to residues T⁵⁷³–R⁵⁸⁶ of the F3 module 1 (SEQ ID NO: 9) (termed the EF loop peptide). However, binding of monomeric forms of these peptides cannot be detected by SPR. Therefore, there were synthesized dendrimeric versions of the peptides in which four peptide sequences of one type (such as SEQ ID NO: 1 or SEQ ID NO: 9) were connected to a three-lysine backbone through their C-termini. This made it possible for the peptide to bind to several molecules of FGFR simultaneously, thus greatly increasing the apparent affinity of the peptides, and, at the same time, increasing the sensitivity of the SPR analysis four fold (since the molecular weight of each peptide was increased four times).

As appears from Fig. 3C, the dendrimeric FG loop peptide binds to FGFR with an apparent K_d of 2.58 ± 2.06 μ M (the coefficients of association and dissociation being $2.07 \pm 1.08 \times 10^3$ M⁻¹s⁻¹ and $3.97 \pm 2.29 \times 10^{-3}$ s⁻¹, respectively). Since binding of the F3 modules 1, 2 to FGFR could be inhibited by ATP and since the peptide contains the entire nucleotide binding motif of NCAM, it was also tested if ATP could interfere with binding of the peptide to FGFR. Indeed, adding 10 mM ATP to 34 μ M peptide inhibited the binding by approx. 70% (Fig. 3C). Fig. 4 demonstrates the real-time binding of the dendrimeric form of the EF loop peptide to FGFR.

These experiments demonstrate that NCAM binding to FGFR can be inhibited by ATP and support the notion that the turn regions between the F and G β -strands of the F3 module 2 and the E and F β -strands of the F3 module 1 are involved in binding to FGFR, and that NCAM sites for FGFR and ATP overlap.

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Assays for determination of FGFR1 phosphorylation and NCAM immunoprecipitation

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Activation of FGFR by the NCAM F3 module 2 and the FG loop peptide

Since the NCAM F3 module 2 and the dendrimeric FG loop peptide bind to FGFR, they may be also expected to induce FGFR activation in living cells. To test this assumption, two assays have been used.

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Assay 1: TREX-293 cells (Invitrogen) were stably transfected with human FGFR1 having a C-terminal StrepII-tag (IBA biotech), using the Flp-In system (Invitrogen). For the study of phosphorylation: $\sim 2 \times 10^7$ cells were starved overnight before stimulation for 20 min with the specified compounds. Cells were lysed in PBS with 1% NP-40 and phosphatase inhibitors cocktail set II (Calbiochem). The cleared cell lysates were incubated with 50 μ l agarose-coupled anti-phosphotyrosine antibodies (4G10-AC, Upstate Biotechnologies) for 3 hrs at 4°C. Care was taken to calibrate the amount of cells employed, so that considerable increases in phosphorylated FGFR could be detected. The bound protein was washed, eluted using 150 mM phenyl phosphate (Sigma), precipitated by 12% trichloroacetic acid, washed in cold acetone and dissolved in SDS-PAGE sample buffer. Immunoblotting was performed using antibodies against the recombinant StrepII-tag (IBA biotech). For immunoprecipitation: $\sim 1 \times 10^7$ cells were transiently transfected with the 180 kDa NCAM isoform or a control vector. Cells were incubated for 24 h and then starved overnight. After lysis, FGFR was purified on a StrepTactin Minicolumn (IBA Biotech) according to the manufacturer's instructions, and analyzed by immunoblotting with polyclonal antibodies against human NCAM.

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As appears from Fig. 5A, both 5 μ M F3 module and 2.5 μ M dendrimeric FG loop peptide substantially increase FGFR phosphorylation compared to the non-stimulated cells.

5 Assay 2: The cDNA for the rat FGFR1 (IIIC isoform) was cloned by RT-PCR using
RNA isolated from the rat PC12 cell line and inserted into a pcDNA3.1(+) plasmid
(Invitrogen), which allows expression of FGFR1 fused to the N-terminal of hexa-
histidine. $\sim 8 \times 10^5$ HEK293 cells were cultured for 24h in 60 mm plates in full medium
10 (DMEM 1965 supplemented with 10% FCS, 100 U/ml penicillin, 100 μ g/ml strepto-
mycin and 58.4 g/l Glutamax) and then transfected with 0.2 μ g plasmid (with FGFR)
using the LipofectAMIN PLUS[™] reagent kit according to the manufacturer's instruc-
tions (Gibco BRL). Cells were grown for another 24 hrs in full medium, and then
shifted to starvation media (DMEM 1965) overnight. FGFR transfected cells were
stimulated for 20 min with the specified compounds, lysed in 8M urea, 1 mM ortho-
15 vanadate (in PBS) and purified from the lysate via the His-tag as follows: The lysate
was loaded on Ni²⁺/NTA-sepharose (Qiagen), washed with lysis buffer plus 10 mM
imidazole, and the FGFR was eluted with lysis buffer plus 250 mM imidazole. The
purified FGFR was analysed by immunoblotting using anti-pentahis (Qiagen) or
anti-phosphotyrosine (PY20, Transduction Laboratories) antibodies. The bands
20 were visualised by chemilumiscense and the band density was measured using a
GeneGnome apparatus (SynGene).

From Fig. 5B, it appears that addition of 5 μ M F3 module 2 or 25 μ M monomeric FG
loop peptide increase FGFR phosphorylation by approx. 150% and 100%, respec-
25 tively, compared to control cells.

Co-immunoprecipitation of NCAM and FGFR

Since the binding between the NCAM and FGFR fragments could be demonstrated
30 *in vitro* by SPR and NMR analyses it was of interest to confirm that native NCAM
binds to FGFR in the living cells. Therefore, TREX-293 cells, stably transfected with
FGFR containing a C-terminal StrepII-tag, were transiently transfected with the 180
kDa NCAM isoform. After lysing the cells, FGFR was affinity purified via the StrepII-
tag and analyzed by immunoblotting using antibodies against NCAM. As appears

from Fig. 5C, NCAM is indeed precipitated by FGFR, thus supporting our SPR and NMR experiments.

Assay for measurement of neurite length of hippocampal neurons stimulated with the F3 module 2, the FG loop or EF loop peptide

Dissociated neurons from embryonic rat hippocampus (embryonic day 19), prepared as described (Skladchikova et al., 1999), were grown on Permanox plastic (Nunc) for 24 h at a density of 6000 cells/cm², at 37°C, 5% CO₂ in Neurobasal medium containing 20 mM Hepes, 100 U/ml penicillin, 100 µg/ml streptomycin, 0.4% BSA supplemented with B27 (Gibco BRL) and the below specified compounds. After 24 h, cells were fixed with paraformaldehyde, stained with Coomassie Brilliant Blue R250 and the length of neurites was measured as described (Skladchikova et al., 1999).

As can be seen from Fig. 6A,B, 5 µM F3 module 2 substantially increased the length of neurites compared to the non-stimulated neurons. The effect was quantified in a dose-response study (Fig. 6C) demonstrating that the F3 module, the FG loop peptide and a truncated version of the peptide (A⁷⁷ – K⁸³) all induced neurite outgrowth with a bell-shaped curve typical of growth factor induced neuritogenesis (Hatten et al., 1988). The potency of the peptides was lower than that of the module, since a 10 times higher concentration was required for maximum effect, and the truncated form was less efficient than the extended form. The stimulatory effect of the F3 module and the FG loop peptide could be completely abrogated by an inhibitor of NCAM-stimulated neurite outgrowth, an antibody against FGFR (Williams et al., 1994) (Fig. 6D), further supporting the notion that the module and the FG loop peptide interact with FGFR. The EF loop peptide of the F3 module 2 was also capable to stimulate the neurite outgrowth significantly. As it appears from Fig. 7 the neurite outgrowth stimulation by the peptide was specifically blocked by an inhibitor of FGFR1, SU54402.

To determine the functionally important amino acids of the FG loop peptide, it was analyzed by truncations and Ala substitutions of various amino acids. Two truncated versions (from the N- and C-terminal) of the FG loop peptide were produced: the nonamer V⁷⁶ – S⁸⁴ and the heptamer Ala⁷⁷ – K⁸³. Both of the truncated peptides re-

tained approximately 50% of the stimulatory effect of the entire FG loop peptide (Fig. 6E), indicating that the turn region between the F and G β -strands is important for the NCAM-FGFR interaction. As can be seen from Fig. 6E, substitution of any amino acid in the heptameric peptide with Ala resulted in a decrease of the neuritogenic potency and a complete loss of function was achieved if E⁷⁸, N⁷⁹, Q⁸⁰, G⁸², K⁸³ were substituted, indicating that these residues are important for interaction with FGFR. Substitution of both Q⁸⁰ and Q⁸¹ from the turn region of the FG loop with Ala in the entire FG loop peptide also completely inactivated the peptide (Fig. 6E). These findings corroborate the NMR experiments showing that N⁷⁸, Q⁸¹, G⁸² and K⁸³ were perturbed in the F3 module 2 by binding to the FGFR Ig module 3. However, when the residues which seem to be important for interaction with ATP (Y⁷⁴, K⁸³ and K⁸⁵) were substituted with Ala in the FG loop peptide, the peptide retained about 60% of the stimulatory effect of the non-mutated peptide (Fig. 6E).

Furthermore, the structure of the heptameric peptide in the F3 module was compared to the known structure of a natural ligand of FGFR, FGF2 (PDB code: 4FGF, Eriksson *et al.*, 1993), and it was found that the peptide exhibited a striking structure and sequence similarity to a loop region in FGF2, A⁴² – R⁴⁸ (Fig. 8A). The conformations of the backbone atoms of the two peptides are virtually identical, with the side chains also having similar conformations. The only exception is R⁴⁸ (in FGF2) whose side chain has a somewhat different conformation from that of K⁸³. As can be seen from Fig. 8B, the peptide derived from FGF2 induced neurite outgrowth to the same extent as the similar NCAM peptide, and substitution of any amino acid with Ala resulted in a complete loss of function. The close sequence and structure similarity between the FG loop of the NCAM F3 module 2 and a part of FGF2 further corroborate the present contention that the former is directly interacting with FGFR.

Since ATP can inhibit the NCAM-FGFR binding and interfere with the FGFR activation by the F3 module 2 and, it may consequently affect the neuritogenic activity of the module. To test this assumption, neurons were stimulated with the below described compounds in the presence of ATP or AMP-PCP. As can be seen from Fig. 9, both ATP and AMP-PCP substantially reduced the neuritogenic effect induced by the F3 module 2 and the FG loop peptide. A complete inhibition of the effect of both the F3 module and the FG loop peptide was achieved when AMP-PCP was added, whereas only the effect of the FG loop peptide was completely inhibited when ATP

was added, indicating that ATP is a less potent inhibitor than its non-hydrolysable analogue. Most significantly, when the amino acid residues of the FG loop peptide presumed to be of importance for ATP binding (Y⁷⁴, K⁸³ and K⁸⁵) were substituted with Ala, the peptide retained its neuritogenic potency, but the stimulatory effect of the peptide could no longer be inhibited by ATP (Fig. 9), supporting the notion that ATP binding regulates the interaction between the F3 module and FGFR.

These results shows that activation of FGFR in neurons by the NCAM F3 module 2, the FG loop and EF loop peptides induce neuritogenesis and that this effect can be inhibited by ATP or a ATP analogue.

Claims

- 5 1. A method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising
- 10 i) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with said receptor and said polypeptide interaction,
- 15 ii) adding the compound of step (i) to the at least two different proteins.
2. The method according to claim 1, wherein the at least two proteins are heterologous.
- 20 3. The method according to claims 1 or 2, wherein at least one of the at least two proteins comprises at least two immunoglobulin (Ig)-like domains and/or at least two fibronectin type 3 (F3) domains, or at least one Ig-like and one F3 domain.
- 25 4. The method according to claim 1, wherein the cell-surface receptor is selected from the family of fibroblast growth factor receptors (FGFRs) comprising FGFR1, FGFR2, FGFR3 or FGFR4.
- 30 5. The method according to claim 4, wherein the fibroblast growth factor receptor is FGFR1 having the amino acid sequence set forth in Swiss-Prot Seq Nos: Q9QZM7, Q99AVV7, Q9UD50 or Q63827, or fragments, or variants thereof, or a functional homologue of said receptor.
- 35 6. The method according to claim 1, wherein the polypeptide is selected from the group comprising transmembrane, cell-surface-associated, extracellular matrix-associated and soluble proteins.

7. The method according to claims 1 or 6, wherein the polypeptide is selected from the group comprising cell adhesion molecules, cell-surface receptors, heparan sulphate proteoglycans, and metalloproteases, extracellular matrix molecules or growth factors.

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8. The method according to the claim 7, wherein the cell adhesion molecule is selected from the group comprising

- Neural Cell Adhesion Molecule (NCAM) (Swiss-Prot Ass. Nos: P13591, P13595-01, P13595),

10 - Neural cell adhesion molecule L1 (Swiss-Prot Ass. Nos: Q9QYQ7, Q9QY38, P11627, Q05695, P32004),

- Neural Cell Adhesion Molecule-2 (NCAM-2) (Swiss-Prot Ass. No: P36335)

- Neuron-glia Cell Adhesion Molecule (Ng-CAM) (Swiss-Prot Ass. No: Q03696; Q90933),

15 - Neural cell adhesion molecule CALL (Swiss-Prot Ass. No: O00533),

- Neuroglian (Swiss-Prot Ass. No: P91767, P20241),

- Nr-CAM (HBRAVO, NRCAM, NR-CAM 12) (Swiss-Prot Ass. Nos: Q92823, O15179, Q9QVN3

- Axonin-1/TAG-1 (Swiss-Prot Ass. Nos: Q02246, P22063, P28685),

20 - Axonal-associated Cell Adhesion Molecule (AxCAM) (NCBI Ass. No: NP_031544.1; Swiss-Prot Ass. No: Q8TC35),

- Myelin-Associated Glycoprotein (MAG) (Swiss-Prot Ass. No: P20917),

- Neural cell adhesion molecule BIG-1 (Swiss-Prot Ass. No: Q62682),

- Neural cell adhesion molecule BIG-2 (Swiss-Prot Ass. No: Q62845),

25 - Fasciclin (FAS-2) (Swiss-Prot Ass. No: P22648),

- Neural cell adhesion molecule HNB-3/NB-3 (Swiss-Prot Ass. Nos: Q9UQ52, P97528, Q9JMB8)

- Neural cell adhesion molecule HNB-2/NB-2 (Swiss-Prot Ass. Nos: O94779, P07409, P97527),

30 - Cadherin (Swiss-Prot Ass. No: Q9VW71),

- Junctional Adhesion Molecule-1 (JAM-1) (Swiss-Prot Ass. Nos: Q9JKD5, O88792),

- Neural cell adhesion F3/F11(Contactin) (Swiss-Prot Ass. Nos: Q63198, P1260, Q12860, Q28106, P14781, O93250),

35 - Neurofascin (Swiss-Prot Ass. Nos: Q90924, Q91Z60; O42414),

- B-lymphocyte cell adhesion molecule CD22 (Swiss-Prot Ass. Nos: Q9R094, P20273),
 - Neogenin (NEO1) (Swiss-Prot Ass. Nos: Q92859, P97603, Q90610, P97798),
 - Intercellular Cell Adhesion Molecule-5 (ICAM-5/telencephalin) (Swiss-Prot Ass. Nos: Q8TAM9, Q60625) or
 - Galactose binding lectin-12 (galectin-12) (Swiss-Prot Ass. Nos: Q91VD1, Q9JKX2, Q9NZ03),
 - Galactose binding lectin-4 (galectin-4) (Swiss-Prot Ass. No: Q8K419; P38552), or fragments, or variants thereof.
9. The method according to the claim 7, wherein the functional cell-surface receptor is selected from the group comprising
- Fibroblast Growth Factor Receptor 1 (FGFR1) (Swiss-Prot Ass. Nos: Q9QZM7, Q99AVV7, Q9UD50, Q63827),
 - Fibroblast Growth Factor Receptor 2 (FGFR2) (Swiss-Prot Ass. Nos: Q96KM2, P21802, Q63241),
 - Fibroblast Growth Factor Receptor 3 (FGFR3) (Swiss-Prot Ass. Nos: Q95M13, AF487554, Q99052),
 - Fibroblast Growth Factor Receptor 4 (FGFR4) (Swiss-Prot Ass. No: Q91742),
 - Neurotrophin Tyrosin Kinase Type-2 (NTRKT-2) (Swiss-Prot Ass. No: Q8WXJ5),
 - Leukocyte Antigen Related Protein-Tyrosine Phosphatase (LAR-PTPRF) (Swiss-Prot Ass. Nos: Q9EQ17, Q64605, Q64604, Q9QW67, Q9VIS8 P10586),
 - Nephlin (Swiss-Prot Ass. Nos: Q925S5, Q9JIX2, Q9ET59, Q9R044, Q9QZS7, Q06500),
 - Protein-Tyrosine Phosphatase Receptor type S (PTPRS) (Swiss-Prot Ass. Nos: Q64699, Q13332, O75870),
 - Protein-Tyrosine Phosphatase Receptor type kappa (R-PTP-kappa) (Swiss-Prot Ass. No: Q15262),
 - Protein-Tyrosine Phosphatase Receptor type D (PTPRD) (Swiss-Prot Ass. Nos: Q8WX65, Q9IAJ1, P23468, Q64487),
 - Ephrin type-A receptor 8 (EPHA8/Tyrosine-Protein Kinase Receptor EEK) (Swiss-Prot Ass. Nos: O09127, P29322),
 - Ephrin type-A receptor 3 (EPHA8/Tyrosine-Protein Kinase Receptor ETK-

- 1/CEK4) (Swiss-Prot Ass. No: P29318),
- Ephrin type-A receptor 2 (Swiss-Prot Ass. No: Q8N3Z2)
 - Insulin Receptor (IR) (Swiss-Prot Ass. No: Q9PWN6)
 - Insulin-like Growth Factor-1 Receptor (IGF-1) (Swiss-Prot Ass. Nos: Q9QVW4, P08069, P24062, Q60751, P15127, P15208)
 - Insulin-related Receptor (IRR) (Swiss-Prot Ass. No: P14616),
 - Tyrosine-Protein Kinase Receptor Tie-1 (Swiss-Prot Ass. Nos: 06805, P35590, Q06806),
 - Roundabout receptor-1 (robo-1) (Swiss-Prot Ass. Nos: O44924, AF041082, Q9Y6N7),
 - Neuronal nicotinic acetylcholine receptor alpha 3 subunit (CHRNA3) (Swiss-Prot Ass. Nos: Q8VHH6, P04757, Q8R4G9, P32297)
 - Neuronal acetylcholine receptor alpha 6 subunit (Swiss-Prot Ass. Nos: Q15825, Q9R0W9)
 - Platelet-Derived Growth Factor Receptor Beta (PDGFRB) (Swiss-Prot Ass. Nos: Q8R406, Q05030),
 - Interleukin-6 Receptor (IL-6R) (Swiss-Prot Ass. No: Q00560),
 - Interleukin-23 Receptor (IL-23R) (Swiss-Prot Ass. No: AF461422),
 - Beta-common cytokine receptor of IL-3, IL5 and GmCsf (Swiss-Prot Ass. No: P32927)
 - Cytokine Receptor-Like molecule 3 (CRLF1) (Swiss-Prot Ass. No: Q9JM58),
 - Class I Cytokine Receptor (ZCYTOR5) (Swiss-Prot Ass. No: Q9UHH5)
 - Netrin-1 receptor DCC (Swiss-Prot Ass. No: P43146),
 - Leukocyte Fc Receptor-like Protein (IFGP2) (Swiss-Prot Ass. Nos: Q96PJ6, Q96KM2),
 - Macrophage Scavenger Receptor 2 (MSR2) (Swiss-Prot Ass. No: Q91YK7), or
 - Granulocyte Colony Stimulating Factor Receptor (G-CSF-R) (Swiss-Prot Ass. No: Q99062),
- or fragments, or variants thereof.
10. The method according to the claim 7, wherein the heparan sulphate proteoglycan is perlecan (Swiss-Prot Ass. No: P98160), or a fragment, or a variant thereof.

11. The method according to the claim 7, wherein the metalloprotease is selected from the group comprising
- ADAM-8 (Swiss-Prot Ass. No: Q05910),
 - ADAM-19 (Swiss-Prot Ass. Nos: Q9H013, O35674),
 - 5 - ADAM-8 (Swiss-Prot Ass. No: P78325),
 - ADAM-12 (Swiss-Prot Ass. Nos: O43184, Q61824),
 - ADAM-28 (Swiss-Prot Ass. Nos: Q9JLN6, Q61824, Q9XSL6, Q9UKQ2),
 - ADAM-33 precursor (Swiss-Prot Ass. Nos: Q8R533, Q923W9),
 - ADAM-9 (Swiss-Prot Ass. Nos: Q13433, Q61072),
 - 10 - ADAM-7 (Swiss-Prot Ass. NoS: Q9H2U9, O35227, Q63180),
 - ADAM-1A Fertilin alpha (Swiss-Prot Ass. No: Q8R533),
 - ADAM-15 (Swiss-Prot Ass. Nos: Q9QYV0, O88839, Q13444),
 - Metalloproteinase-desintegrin domain containing protein (TECAM) (Swiss-Prot Ass. No: AF163291),
 - 15 - Metalloproteinase 1 (Swiss-Prot Ass. Nos: O95204, Q9BSI6),
- or fragments, or variants thereof.
12. The method according to the claim 7, wherein the extracellular matrix molecule is selected from the group comprising
- 20 - Collagen type VII (Swiss-Prot Ass. No: Q63870),
 - Fibronectin (Swiss-Prot Ass. Nos: Q95KV4, Q95KV5, P07589, Q28377, U42594, O95609, P11276), or
 - Tenascin-R (Swiss-Prot Ass. Nos: Q15568, O00531, Q90995, P10039),
 - 25 or fragments, or variants thereof.
13. The method according to the claim 7, wherein the growth factor is Cytokine-like factor-1 (CLF-1) (Swiss-Prot Ass. No: O75462), or a fragment, or a variant thereof.
14. The method according to claim 1, wherein the interaction between the at least two different proteins is a low affinity interaction.
15. The method according to claim 14, wherein the affinity of interaction is within the range of K_d 10^{-3} - 10^{-11} M.

16. The method according to claim 1, wherein the compound is any compound capable of binding to at least one of the at least two different proteins.
17. The method according to claim 16, wherein the compound is selected from the group comprising peptides, carbohydrates, lipids, or nucleotides.
18. The method of claim 17, wherein the peptide comprises any of the amino acid sequences set forth on SEQ ID NOS: 2-10, 100, 125 or variants, or fragments of said sequences, or a combination of said sequences.
19. The method of claim 17, wherein the peptide comprises a contiguous amino acid sequence having at least 60% homology to any of the sequences set forth in SEQ ID NOS: 2-10, 100, 125, or a variant of said amino acid sequence, or a fragment of said amino acid sequence.
20. The method of claim 17, wherein the peptide comprises any of the amino acid sequences set forth in SEQ ID NOS: 11-99, 101-124, 126-146 or variants, or fragments of said sequences, or a combination of said sequences.
21. The method of claim 17, wherein the peptide encompasses a sequence of at least 6 to 16 contiguous amino acids capable of forming a strand-loop-strand fold.
22. A method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein said binding site is essentially consisting of one or more "strand-loop-strand" structural motifs, comprising
- iii) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with said receptor and said polypeptide interaction,
 - iv) adding the compound of step (i) to the at least two different proteins.

23. The method according to claim 22, wherein the binding site consisting of one or more "strand-loop-strand" structural motifs.
- 5 24. The method according to claims 22 or 23 further comprising at least one feature any of the claims 1-21.
- 10 25. A screening method for a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising
- 15 i) providing the at least two different proteins;
ii) providing the compound;
iii) adding the compound to the at least two different proteins;
iv) determining whether the interaction between the at least two different proteins has been modulated,
- 20 v) selecting the compound capable of modulating the interaction between the at least two different proteins.
- 25 26. The screening method according to claim 25, wherein the functional cell-surface receptor is selected from the group as defined in claims 4-5.
27. The screening method according to claim 25, wherein the polypeptide is selected from the group comprising polypeptides as defined in any of the claims 6-13.
- 30 28. The screening method according to claim 27, wherein the polypeptide, is NCAM having the amino acid sequence set forth in Swiss-Prot Seq Nos: P13591, P13595-01 or P13595, or fragments, or variants thereof, a functional homologue of NCAM.

29. The screening method according to claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of normal, degenerated or damaged NCAM presenting cells.
- 5 30. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament treatment of diseases and conditions of the central and peripheral nervous system, or of the muscles or of various organs.
- 10 31. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic damage, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, 15 nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression; for treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as after organ transplantation, or such as genetic or traumatic atrophic muscle disorders; or for treatment of diseases or conditions of various organs, such as degenerative conditions of the gonads, of the pancreas such as 20 diabetes mellitus type I and II, of the kidney such as nephrosis and of the heart, liver and bowel.
- 25 32. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, nerve 30 degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression.
- 35 33. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the promotion of wound-healing.

34. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of cancer.
- 5 35. The screening method according to claim 31, wherein the cancer is any type of solid tumors requiring neoangiogenesis.
- 10 36. The screening method according to the claims 25-28, wherein the first compound is for the manufacture of a medicament for the prevention of cell death of heart muscle cells, such as after acute myocardial infarction, or after angiogenesis.
- 15 37. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for revascularisation.
- 20 38. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the stimulation of the ability to learn and/or the short and/or long-term memory.
- 25 39. An assay for sequential screening of a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of
- 30 i) providing the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragments or a variants of said homologues,

- ii) adding the at least one receptor molecule of step (i) to the at least one polypeptide of step (i), or adding the at least one polypeptide of step (i) to the at least one receptor molecule of step (i) and permitting the interaction between the said receptor and said polypeptide, followed by the
- 5 iii) recording the interaction between the molecules of step (ii),
iv) adding the candidate compound to the molecules of step (ii);
v) recording the interaction between the molecules of step (iv), followed by the
vi) assessment of at least one effect of the candidate compound on the interaction between the molecules of step (iv), followed by the
- 10 vii) selection of a compound capable of modulating the interaction between the at least one functional cell-surface receptor molecule and the at least one polypeptide of step (i).
40. The assay according to claim 39, wherein step (vii) is followed by the steps of
- 15 viii) adding the selected in step (vii) candidate compound to at least one cell presenting the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or
- 20 variants, or homologues of said sequences, or a fragments or a variants of said homologues with, and
- ix) assessing at least one effect of the compound on the cell of step (viii).
41. The assay according to claims 39 and 40, wherein the recording of interaction
- 25 between the molecules on step (iii) or step (v), and the assessment of the at least one effect of the candidate compound on step (vi) is achieved by using a method selected from the group comprising surface plasmon resonance, nucleic magnetic resonance, sedimentation, immunoprecipitation, two-hybrid system, or resonance energy transfer.
- 30
42. The assay according to claim 40, wherein the at least one effect of step (ix) is being selected from promotion/inhibition of receptor phosphorylation, intracellular signal transduction, gene expression, cellular adhesion, cell motility, neuritegenesis, apoptosis, cell proliferation or synaptic plasticity.
- 35

43. A method for molecular design for a compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146; or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues comprising using structural data on the binding site of NCAM with FGFR.
44. A method for isolating a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of
- i) providing a method for sequential screening the candidate compound as defined in claim 39 and/or
 - ii) providing a method for molecular design of the candidate compound as defined in claim 43,
 - iii) isolating the candidate compound.
45. A peptide fragment having any of the following amino acid sequences:
- NIEVWVEAENALGKKV (SEQ ID NO: 2),
ATNRQGKVKAF AHL (SEQ ID NO: 3),
RYVELYVVADSQEFQK (SEQ ID NO: 4),
VAENSRGKNVAKG (SEQ ID NO: 5),
GEYWCV AENQYGQR (SEQ ID NO: 6),
RLAALNGKGLGEIS (SEQ ID NO: 7),
KYIAENMKAQNVAKEI (SEQ ID NO: 8),
TIMGLKPETRYAVR (SEQ ID NO: 9),
KGLGEISAATEFKT (SEQ ID NO: 10),
NMGIWVQAENALG (SEQ ID NO: 11),

IWVQAENMLG (SEQ ID NO: 12),
EIWVEATNRLG (SEQ ID NO: 13),
VWVQAANALG (SEQ ID NO: 14),
EVWIEKDPAKGRI (SEQ ID NO: 15),
5 ATNKGGEVKKNGHL (SEQ ID NO: 16),
KYVELYLVDYLEFQK (SEQ ID NO: 17),
RYVELYVVDNAEFQ (SEQ ID NO: 18),
KYVELVIVADNREFQR (SEQ ID NO: 19),
KYIEYYLVDNGEFKR (SEQ ID NO: 20),
10 RYLELYIVADHTLF (SEQ ID NO: 21),
KYVEMFVVVNHQRFQ (SEQ ID NO: 22),
RYVELFIVVDKERY (SEQ ID NO: 23),
KYVELFIVADDTVYRR (SEQ ID NO: 24),
KFIELFVVADEYVYRR (SEQ ID NO: 25),
15 KIVEKVIVADNSEVRK (SEQ ID NO: 26),
VELVIVADHSEAQK (SEQ ID NO: 27),
VAENSRGKNIAKG (SEQ ID NO: 28),
IAENSRGKNVARG (SEQ ID NO: 29),
AENSRGKNSFRG (SEQ ID NO: 30),
20 IASNLGRNLAKG (SEQ ID NO: 31),
IPENSLGKTYAKG (SEQ ID NO: 32),
IAENMKAQNEAK (SEQ ID NO: 33),
QFIAENMKSHNETKEV (SEQ ID NO: 34),
GEYWCVAKNRVGQ (SEQ ID NO: 35),
25 GSYTCVAENMVĠK (SEQ ID NO: 36),
GKYVCVGTNMVGER (SEQ ID NO: 37),
GNYTCVENEY G (SEQ ID NO: 38),
GEYTCLAGNSIG (SEQ ID NO: 39),
QYYCVAENGYG (SEQ ID NO: 40),
30 GEYYQAEQNGYG (SEQ ID NO: 41),
GNYTCLVENEY G (SEQ ID NO: 42),
GMYQCLAENAYG (SEQ ID NO: 43),
GMYQCAENTHG (SEQ ID NO: 44),
GIYYCLASNNGY (SEQ ID NO: 45),
35 GGYCTADNSYG (SEQ ID NO: 46),

5 GEYQCFARNDYG (SEQ ID NO: 47),
GEYFCLASNKMG (SEQ ID NO: 48),
GEYQCFARNKFG (SEQ ID NO: 49),
GEYFCLASNKMG (SEQ ID NO: 50),
GGYYCTADNNYG (SEQ ID NO: 51),
GNYSCEAENAWGTK (SEQ ID NO: 52),
GEYTCLAENSLG (SEQ ID NO: 53),
GEYECVAENGR LG (SEQ ID NO: 54),
GNYTCVVENKFGR (SEQ ID NO: 55),
10 GEYTCLAGNSIG (SEQ ID NO: 56),
GEYFCVASNPIG (SEQ ID NO: 57),
EYTCIANNQAGE (SEQ ID NO: 58),
GMYQCVAENKHLG (SEQ ID NO: 59),
GEYMCTASNTIGQ (SEQ ID NO: 60),
15 EYVCIAENKAGEQ (SEQ ID NO: 61),
GDYTLIAKNEYGK (SEQ ID NO: 62),
GFYQCVAENEAG (SEQ ID NO: 63),
GKYECVATNSAGTR (SEQ ID NO: 64),
GEYFCVYNNSLG (SEQ ID NO: 65),
20 GEYECATNAHGR (SEQ ID NO: 66),
GAYWCQGTNSVGK (SEQ ID NO: 67),
GTYSCVAENILG (SEQ ID NO: 68),
RVAAVNGKGQGDYS (SEQ ID NO: 69),
RVAaingCGIGPFS (SEQ ID NO: 70),
25 AVLNGKGLG (SEQ ID NO: 71),
ALNGQGLGATS (SEQ ID NO: 72),
RLAAKNRAGLGE (SEQ ID NO: 73),
RLGVVTGKDLGEI (SEQ ID NO: 74),
TVTGLKPETSYMVK (SEQ ID NO: 75),
30 TLTGLKPSTRYRI (SEQ ID NO: 76),
TLTGLQPSTRYRV (SEQ ID NO: 77),
TLLGLKPDTTYDIK (SEQ ID NO: 78),
TLQGLRPETAYELR (SEQ ID NO: 79),
TLRGLRPETAYELR (SEQ ID NO: 80),
35 TLMNLRPKTGYSVR (SEQ ID NO: 81),

TVSGLKPGTRY (SEQ ID NO: 82),
TISGLKPDTTY (SEQ ID NO: 83),
TLQGLKPDYAY (SEQ ID NO: 84),
LRGLKPWTQYAV (SEQ ID NO: 85),
5 IDGLEPDTEYIVR (SEQ ID NO: 86),
LQGLKPWTQYAI (SEQ ID NO: 87),
TITGLEPGTEYTIQ (SEQ ID NO: 88),
GLKPWTQYAV (SEQ ID NO: 89),
TLASLKPWTQYAV (SEQ ID NO: 90),
10 LMGLQPATEYIV (SEQ ID NO: 91),
KGMGPMSEAVQFRT (SEQ ID NO: 92),
TLTGLKPDTTYDVK (SEQ ID NO: 93),
ISGLQPETSYSL (SEQ ID NO: 94),
TLLGLKPDTTYDIK (SEQ ID NO: 95),
15 TISGLTPETTYSI (SEQ ID NO: 96),
GNYSCLAENRLGR (SEQ ID NO: 97),
GNYTCVVENRVG (SEQ ID NO: 98),
GTYHCVATNAHG (SEQ ID NO: 99),
LSHNGVLTGYLLSY (SEQ ID NO: 100),
20 NGVLTGYVLRV (SEQ ID NO: 101),
NGVLTGYNLRY (SEQ ID NO: 102),
NGNLTGYLLQY (SEQ ID NO: 103),
VDENGVLTGYKIYY (SEQ ID NO: 104),
THNGALVGYSVRY (SEQ ID NO: 105),
25 NGILTEYILKY (SEQ ID NO: 106),
NGILIGYTLRY (SEQ ID NO: 107),
THSGQITGYKIRY (SEQ ID NO: 108),
NGKITGYIIYY (SEQ ID NO: 109),
LSHNGIFTLY (SEQ ID NO: 110),
30 NGILTEYTLKY (SEQ ID NO: 111),
LDPNGIITQYEISY (SEQ ID NO: 112),
NGKITGYIIYY (SEQ ID NO: 113),
HLEVQAFNGRGS GPA (SEQ ID NO: 114),
HLTVRAYNGAGYGP (SEQ ID NO: 115),
35 HLSVKAYNSAGTGPS (SEQ ID NO: 116),

HLAVKAYNSAGTGPS (SEQ ID NO: 117),
NLEVRAFNSAGDGP (SEQ ID NO: 118),
HLTVLAYNSKGAGP (SEQ ID NO: 119),
LRVLVFNGRGDGP (SEQ ID NO: 120),
5 HIDVSAFNSAGYGP (SEQ ID NO: 121),
HLAVELFNDR (SEQ ID NO: 122),
LELQSINFLGGQPA (SEQ ID NO: 123),
HFTVRAYNGAGYGP (SEQ ID NO: 124),
HLEVQAFNDRGSQPA (SEQ ID NO: 125),
10 VIADQPTFVKYLIK (SEQ ID NO: 126),
TIKGLRPGVWYEGQ (SEQ ID NO: 127),
TLTELPSTQYTVK (SEQ ID NO: 128),
TLDDLAPDTTYLVQ (SEQ ID NO: 129),
TVSDVTPHAIYTVR (SEQ ID NO: 130),
15 IIRGLNASTRYLFR (SEQ ID NO: 131),
TLMNLRPKTGYSVR (SEQ ID NO: 132),
TLTGLKPGTEYEVR (SEQ ID NO: 133),
GPEHLMPSSTYVAR (SEQ ID NO: 134),
RVTGLTPKKTYEFR (SEQ ID NO: 135),
20 LTGLKPGTEYEFR (SEQ ID NO: 136),
EVRVQAVNGGGNGPP (SEQ ID NO: 137),
LIKVVAINDRGE (SEQ ID NO: 138),
VVSIIAVNGREE (SEQ ID NO: 139),
VSVYAQNQNGE (SEQ ID NO: 140),
25 TISLVAEKGRHK (SEQ ID NO: 141),
HLEVQAFNDRGSGPA (SEQ ID NO: 142),
HVEVQAFNDRGLGPA (SEQ ID NO: 143),
HVEVQAFNDRGLGPA (SEQ ID NO: 144),
EFRVRAVNGAGEG (SEQ ID NO: 145),
30 VARVRTRLAPGSRLS (SEQ ID NO: 146)
or fragments, or variants thereof.

46. A compound comprising at least one peptide fragment having at least one of the
sequences set forth in SEQ ID NO: 2-146 or the sequence of a fragment, or
35 variant, or homologue of said sequences.

47. Use of a peptide fragment as defined in claim 45 and/or compound as defined in claim 42 for the manufacture of a medicament for treatment of conditions as defined in any of the claims 29-38.
- 5
48. An antibody capable of binding to an epitope comprising a binding site to a cell surface receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragment or a variant of said antibody.
- 10
49. An antibody capable of binding to an epitope comprising at least one of the sequences set forth in SEQ ID NOS: 1-146, or a fragment, or a variant of said antibody.
- 15
50. Use of an antibody according to claims 48 or 49 for the modulation of interaction between a cell surface receptor, or a fragment or variant thereof, and a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues.
- 20
51. Use of an antibody as defined in claims 48 or 49 for the manufacture of a medicament for treatment of conditions as defined in any of the claims 29-38.
- 25
52. A method for the production of an antibody as defined in claims 48 and 49 comprising administering to an animal a peptide fragment comprising at least one sequence selected from the sequences set forth in SEQ ID NOS: 1-146.
- 30
53. A method for producing a pharmaceutical composition comprising the steps of claim 39 and further the step of formulating the compound with pharmaceutically acceptable carrier or solvent.

Table 1

Structural precision		RMS deviations from idealized geometry	
RMS deviation for backbone atoms	0.25 Å	bonds	0.0027 ± 0.0000 Å
RMS deviation for heavy atoms	0.68 Å	bond angles	1.4558 ± 0.0075 deg.
		improper bond angles	0.8674 ± 0.0198 deg.
Number of constraints		RMS violation of constraints	
long range NOE	1434:	NOE/hydrogen bonds	0.0189 ± 0.0007 Å
medium range NOE	717	dihedral angles	0.0360 ± 0.0176 deg.
sequential NOE	122		
intra NOE	364	Structure analysis with program WHATCHECK	
dihedral angle	119	2 nd generation packing quality Z score	-1.42 ± 0.17
hydrogen bond	44	Ramachandran plot Z score	-1.94 ± 0.27
	80	χ_1 plot Z score	-1.53 ± 0.34
		backbone conformation Z score	-2.10 ± 0.20
Energies (kcal/mol):		Structure analysis with program PROCHECK	
bonds	2.23 ± 0.05	number of residues in the most favored region of Ramachandran plot	75.3 %
bond angles	191.2 ± 0.08	all of the analyzed main- and side-chain parameters found within normal ranges when compared to X-ray structures of 2Å resolution	
NOE	5.02 ± 0.36		
dihedral angles	0.004 ± 0.005		
hydrogen bonds	-157.5 ± 7.1		
van der Waals	-359.9 ± 7.2		
dihedral bond angles	494.2 ± 11.4		
improper bond angles	24.9 ± 2.2		
overall	164 ± 11.4		

RMS deviations from the average for residues 3-96 in 30 structures. Residues 1-2 are extra residues from the vector DNA. Number of non-redundant constraints. The energies were calculated using the CHARMM force field with force constants for NOE of 10 kcal mol⁻¹ Å and for dihedral constraints of 200 kcal mol⁻¹ rad.

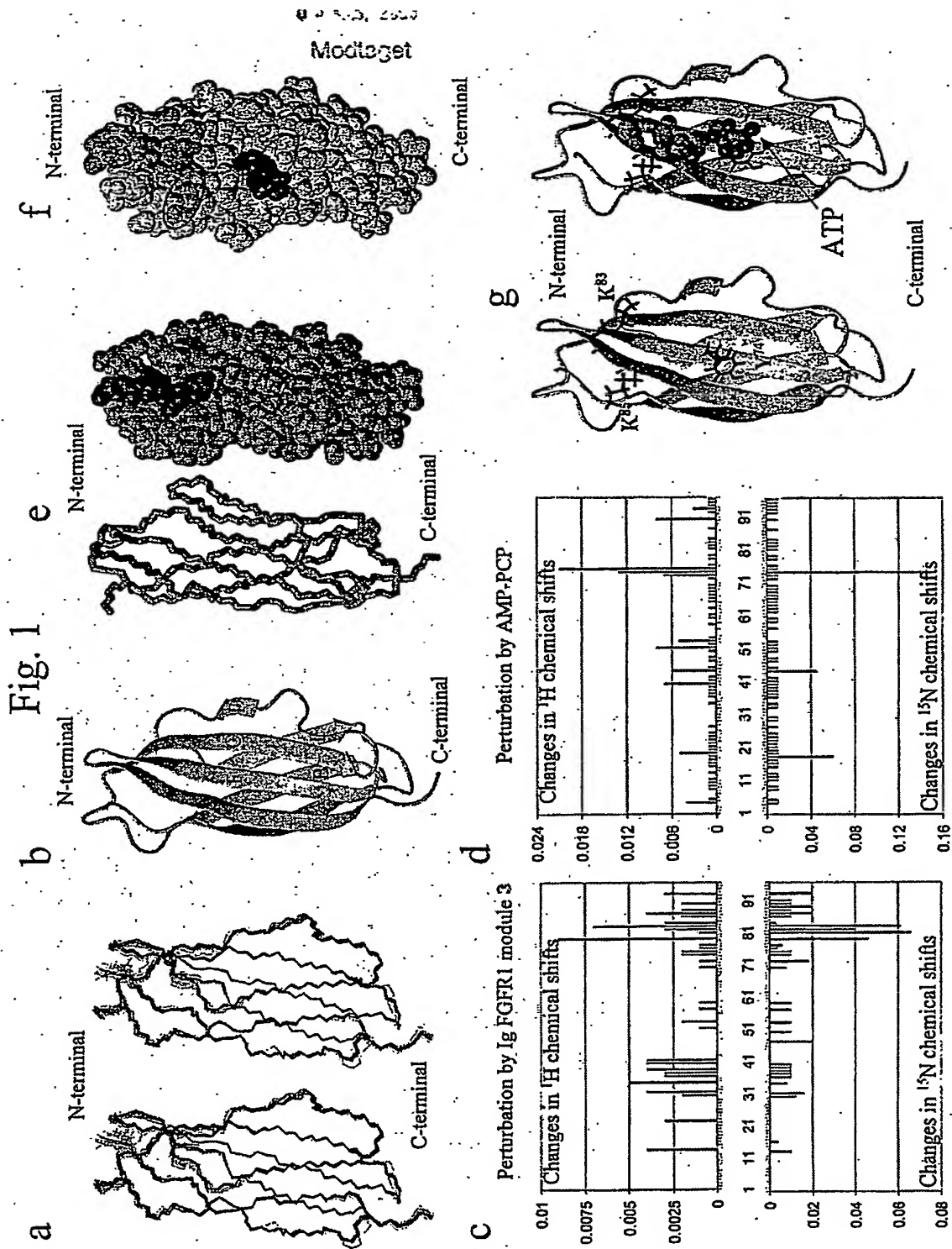


Fig.2

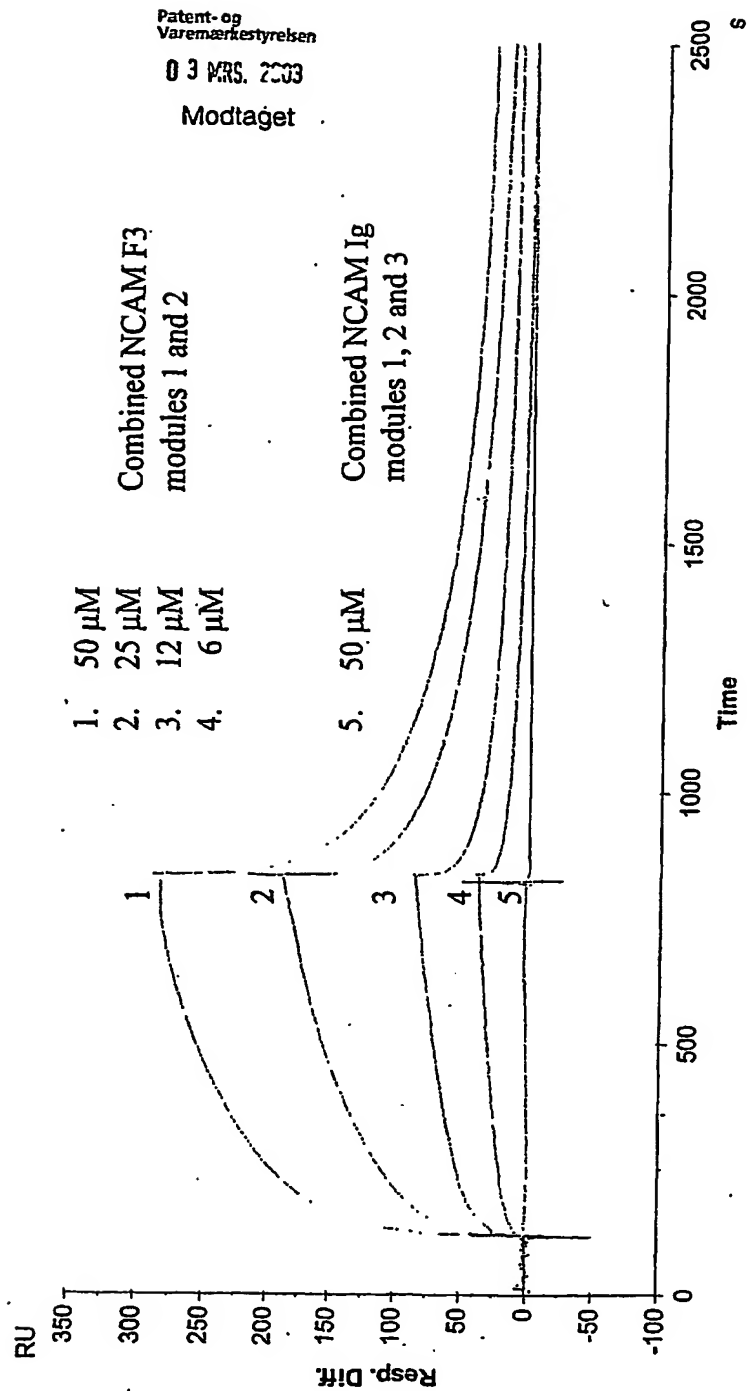
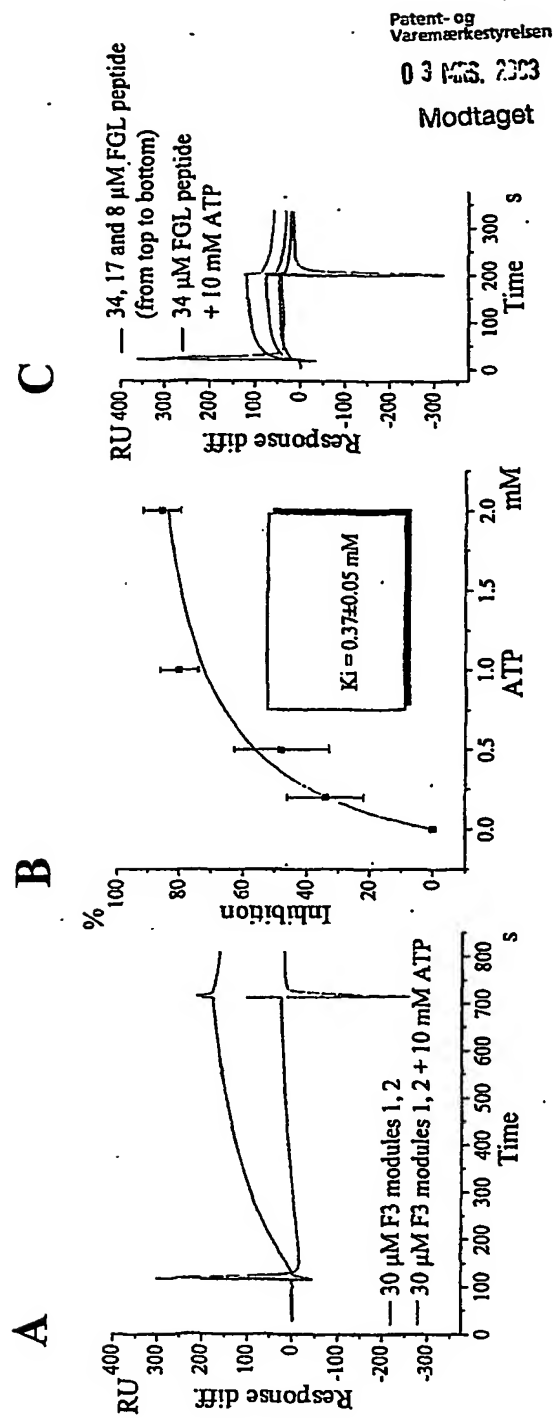


Fig. 3



Patent- og
Varemærkestyrelsen

0 3 MRS. 2333

Modtaget

Fig. 4

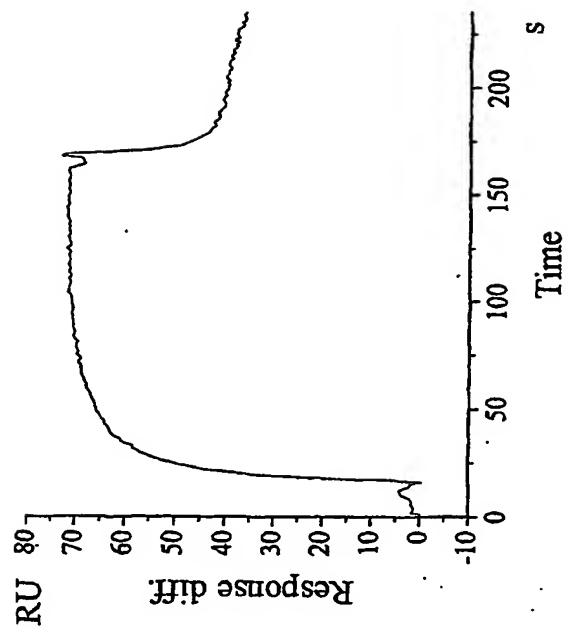
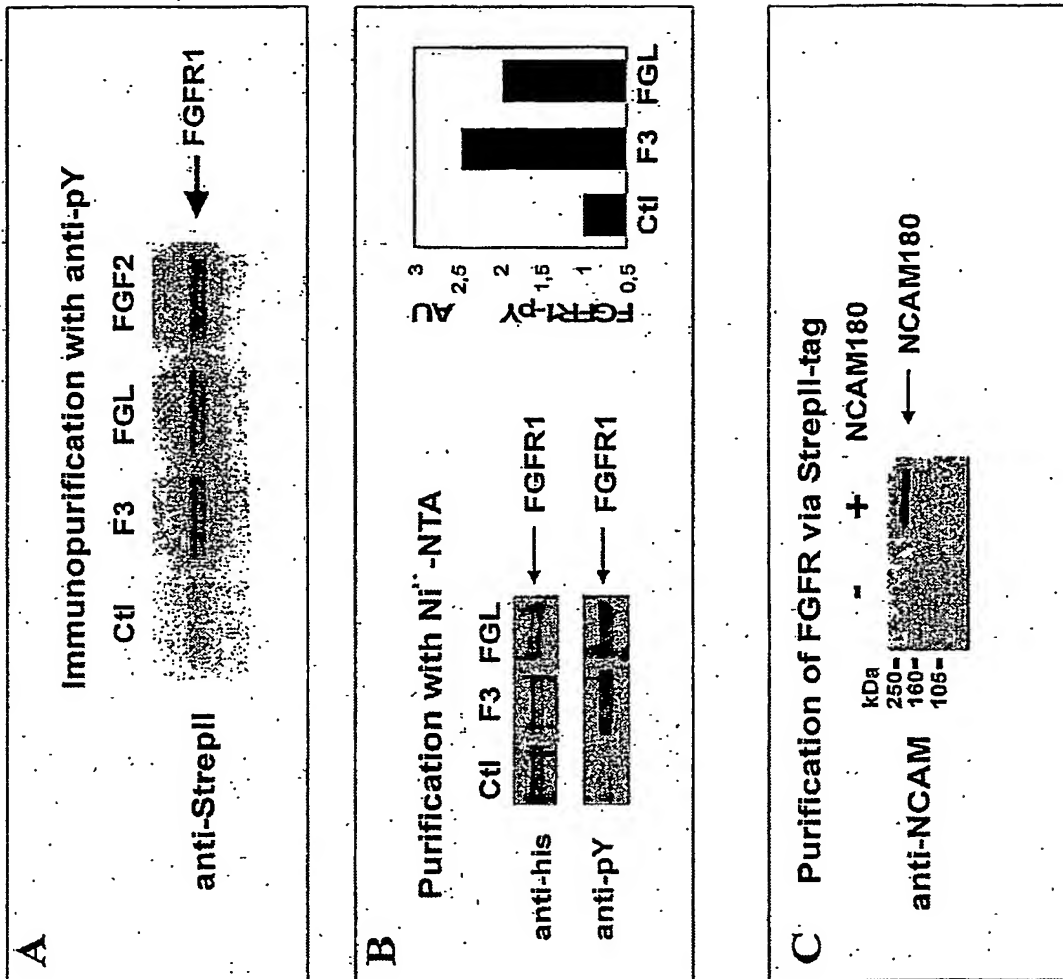


Fig.5



Patent - op
Varemerkingsproven

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Modtager

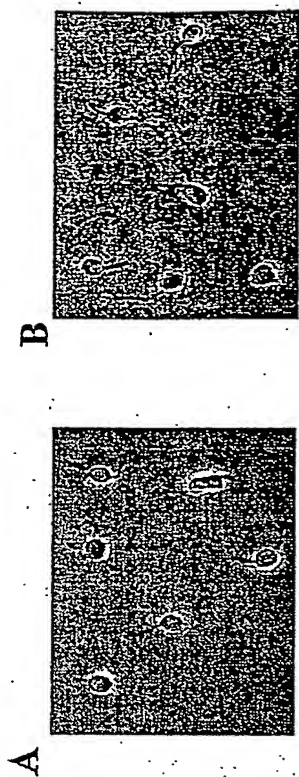
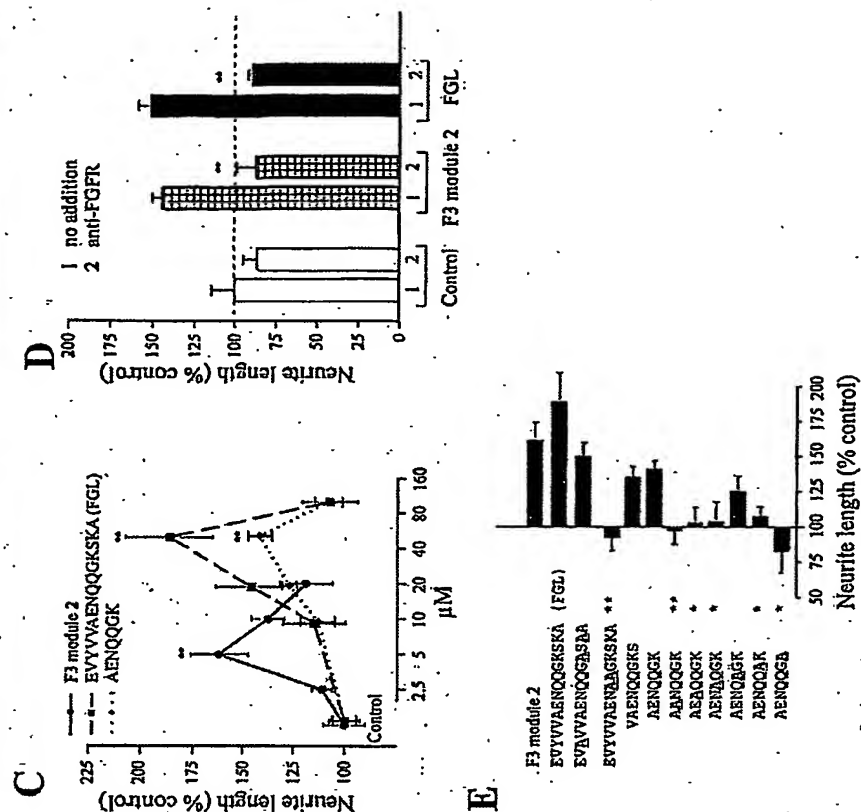


Fig. 6



Detekt - Cq
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Patent- og
Varemærkestyrelsen
03. Marts 2003
Modtaget

Fig. 7

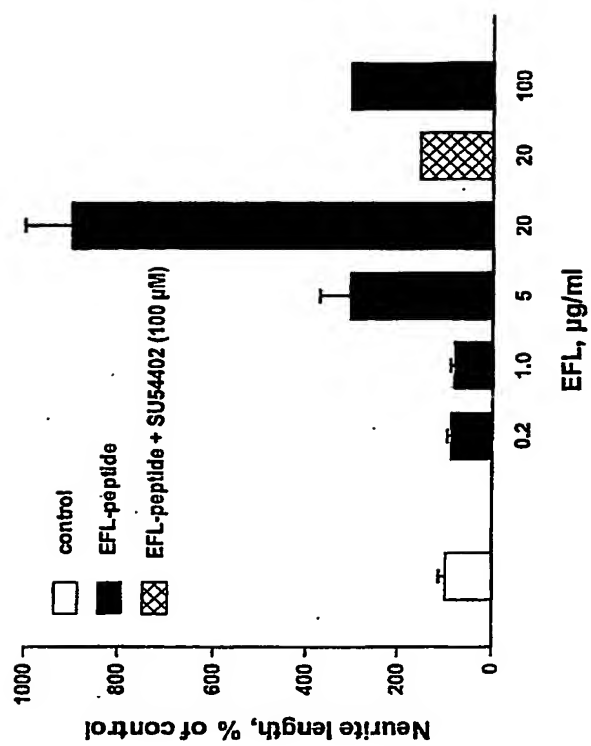


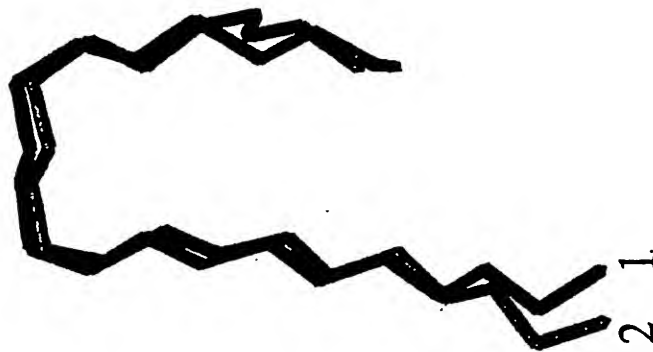
Fig.8

a

AENQQGK - NCAM heptamer (1)

|...::||

AMKEDGR - FGF2 heptamer (2)



b

Modtaget
0 3 FRS, 2303
Patent- og
Videnskabsstyrelsen

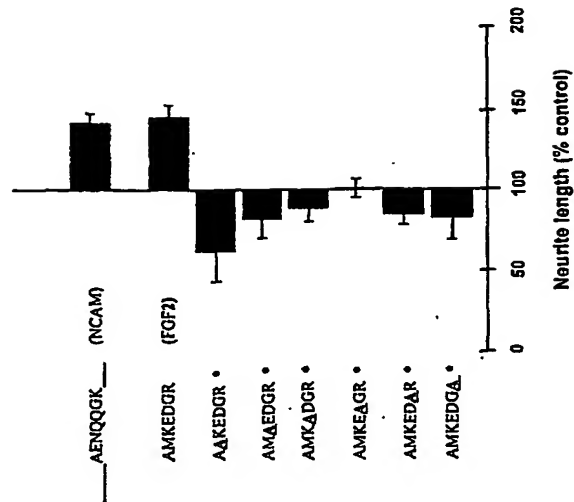
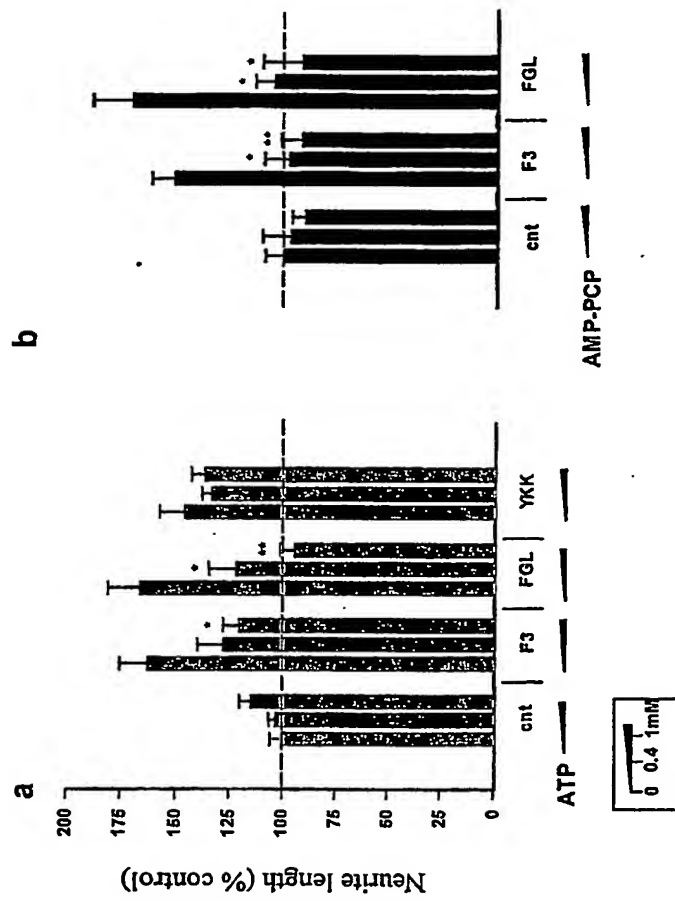


Fig. 9



Patent- og
Varemærkestyrelsen
03.03.2003
Modtaget

SEQUENCE LISTING

Patent- og
Varemærkestyrelsen

03.03.2003

Modtaget

<110> ENKAM Pharmaceutical A/S

<120> Method of modulation of interaction between receptor and
ligand

<130> P 697 DK 01

<160> 146

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> NCAM Fn III, 2 [Swiss-Prot: P13591]: FGFR binding motif

<400> 1

Glu Val Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala
1 5 10 15

<210> 2

<211> 16

<212> PRT

<213> Interleukin-6 receptor beta chain [Swiss-Prot: Q00560]:
FGFR binding motif

<400> 2

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Lys Val
1 5 10 15

<210> 3

<211> 14

<212> PRT

<213> Heparan sulfate proteoglycan perlecan [Swiss-Prot: P98160]:
FGFR binding motif

<400> 3

Ala Thr Asn Arg Gln Gly Lys Val Lys Ala Phe Ala His Leu
1 5 10

<210> 4

<211> 16

<212> PRT

<213> Disintegrin and metalloprotease domain 8 (ADAM-8)
[Swiss-Prot: Q05910]: FGFR binding motif

<400> 4

Arg Tyr Val Glu Leu Tyr Val Val Ala Asp Ser Gln Glu Phe Gln Lys
1 5 10 15

<210> 5

<211> 13

<212> PRT

<213> Axonal-associated cell adhesion molecule [NCBI:
NP_031544.1]: FGFR binding motif

<400> 5

Val Ala Glu Asn Ser Arg Gly Lys Asn Val Ala Lys Gly

1 5 10

<210> 6

<211> 14

<212> PRT

<213> Myelin-associated glycoprotein (MAG) [Swiss-Prot: P20917]:
FGFR binding motif

<400> 6

Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg
1 5 10

<210> 7

<211> 16

<212> PRT

<213> Neuronal nicotinic acetylcholine receptor alpha 3 subunit
(CHRNA3) [Swiss-Prot: Q8VHH6/P04757:/Q8R4G9/P32297]: FGFR binding
motif

<400> 7

Lys Tyr Ile Ala Glu Asn Met Lys Ala Gln Asn Val Ala Lys Glu Ile
1 5 10 15

<210> 8

<211> 14

<212> PRT

<213> FIIII,1 domain of NCAM [Swiss-Prot: P13591]: FGFR binding
motif

<400> 8

Thr Ile Met Gly Leu Lys Pro Glu Thr Arg Tyr Ala Val Arg
1 5 10

<210> 9

<211> 14

<212> PRT

<213> FIII,1 domain of NCAM (Swiss-Prot: P13591): FGFR binding motif

<400> 9

Lys Gly Leu Gly Glu Ile Ser Ala Ala Thr Glu Phe Lys Thr
1 5 10

<210> 10

<211> 13

<212> PRT

<213> Granulocyte colony stimulating factor receptor precursor (G-CSF-R; CD114 antigen) [Swiss-Prot: Q99062]: FGFR binding motif

<400> 10

Asn Met Gly Ile Trp Val Gln Ala Glu Asn Ala Leu Gly
1 5 10

<210> 11

<211> 14

<212> PRT

<213> NCAM Fn III, 1 [Swiss-Prot: P13591]: FGFR binding motif

<400> 11

Arg Leu Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser
1 5 10

<210> 12

<211> 10

<212> PRT

<213> Granulocyte colony stimulating factor receptor precursor
(G-CSF-R; CD114 antigen) [Swiss-Prot: P40223]: FGFR binding motif

<400> 12

Ile Trp Val Gln Ala Glu Asn Met Leu Gly
1 5 10

<210> 13

<211> 11

<212> PRT

<213> Cytokine-like factor-1 precursor (CLF-1) [Swiss-Prot:
O75462]: FGFR binding motif

<400> 13

Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly
1 5 10

<210> 14

<211> 10

<212> PRT

<213> Interleukin-23 receptor (IL-23R) [AF461422]: FGFR binding
motif

<400> 14

Val Trp Val Gln Ala Ala Asn Ala Leu Gly
1 5 10

<210> 15

<211> 13

<212> PRT

<213> Complement factor 1 q , alpha polypeptide (C1QA)
[Swiss-Prot: Q9DCM6]: FGFR binding motif

<400> 15

Glu Val Trp Ile Glu Lys Asp Pro Ala Lys Gly Arg Ile
1 5 10

<210> 16

<211> 14

<212> PRT

<213> Fasciclin II precursor (FAS2) [Swiss-Prot: P22648]: FGFR
binding motif

<400> 16

Ala Thr Asn Lys Gly Gly Glu Val Lys Lys Asn Gly His Leu
1 5 10

<210> 17

<211> 16

<212> PRT

<213> ADAM-19 precursor (EC 3.4.24.-) [Swiss-Prot:
Q9H013/O35674]: FGFR binding motif

<400> 17

Lys Tyr Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln Lys
1 5 10 15

<210> 18

<211> 15

<212> PRT

<213> ADAM-8 precursor (EC 3.4.24.-) [Swiss-Prot: P78325]: FGFR binding motif

<400> 18

Arg Tyr Val Glu Leu Tyr Val Val Val Asp Asn Ala Glu Phe Gln
1 5 10 15

<210> 19

<211> 16

<212> PRT

<213> ADAM-12 precursor (EC 3.4.24.-) [Swiss-Prot: O43184; Q61824]: FGFR binding motif

<400> 19

Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln Arg
1 5 10 15

<210> 20

<211> 16

<212> PRT

<213> Metalloproteinase-disintegrin domain containing protein
TECADAM [AF163291] : FGFR binding motif

<400> 20

Lys Tyr Ile Glu Tyr Tyr Val Val Leu Asp Asn Gly Glu Phe Lys Lys
1 5 10 15

<210> 21

<211> 14

<212> PRT

<213> ADAM-33 precursor (EC 3.4.24.-) [Swiss-Prot: Q9BZ11/Q923W9]:

FGFR binding motif

<400> 21

Arg Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe
1 5 10

<210> 22

<211> 15

<212> PRT

<213> ADAM-1A Fertilin alpha [Swiss-Prot: Q8R533]: FGFR binding motif

<400> 22

Lys Tyr Val Glu Met Phe Val Val Val Asn His Gln Arg Phe Gln
1 5 10 15

<210> 23

<211> 14

<212> PRT

<213> ADAM-9 [Swiss-Prot: Q13433; Q61072]: FGFR binding motif

<400> 23

Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg Tyr
1 5 10

<210> 24

<211> 16

<212> PRT

<213> ADAM-7 precursor [Swiss-Prot: Q9H2U9]: FGFR binding motif

<400> 24

Lys Tyr Val Glu Leu Phe Ile Val Ala Asp Asp Thr Val Tyr Arg Arg
1 5 10 15

<210> 25

<211> 16

<212> PRT

<213> ADAM-7 precursor [Swiss-Prot: O35227; Q63180]: FGFR binding motif

<400> 25

Lys Phe Ile Glu Leu Phe Val Val Ala Asp Glu Tyr Val Tyr Arg Arg
1 5 10 15

<210> 26

<211> 16

<212> PRT

<213> ADAM-15 precursor [Swiss-Prot: Q9QYV0; O88839]: FGFR binding motif

<400> 26

Lys Ile Val Glu Lys Val Ile Val Ala Asp Asn Ser Glu Val Arg Lys
1 5 10 15

<210> 27

<211> 14

<212> PRT

<213> ADAM-15 precursor [Swiss-Prot: Q13444]: FGFR binding motif

<400> 27

Val Glu Leu Val Ile Val Ala Asp His Ser Glu Ala Gln Lys

1 .5 10

<210> 28

<211> 13

<212> PRT

<213> Neural cell adhesion protein BIG-2 precursor [Swiss-Prot: Q62845]: FGFR binding motif

<400> 28

Val Ala Glu Asn Ser Arg Gly Lys Asn Ile Ala Lys Gly
1 5 10

<210> 29

<211> 13

<212> PRT

<213> Neuronal glycoprotein CNTN3 [Swiss-Prot: Q07409]: FGFR binding motif

<400> 29

Ile Ala Glu Asn Ser Arg Gly Lys Asn Val Ala Arg Gly
1 5 10

<210> 30

<211> 12

<212> PRT

<213> NB-2(HNB-2/NB-2), a neural cell recognition molecule of the contactin/F3 subgroup [Swiss-Prot: O94779/P97527]: FGFR binding motif

<400> 30

Ala Glu Asn Ser Arg Gly Lys Asn Ser Phe Arg Gly
1 5 10

<210> 31

<211> 13

<212> PRT

<213> HNB-3/NB-3 [Swiss-Prot: Q9UQ52/P97528/Q9JMB8]: FGFR binding motif

<400> 31

Ile Ala Ser Asn Leu Arg Gly Arg Asn Leu Ala Lys Gly
1 5 10

<210> 32

<211> 13

<212> PRT

<213> Putative fat-like cadherin precursor (Drosophila)
[Swiss-Prot: Q9VW71]: FGFR binding motif

<400> 32

Ile Pro Glu Asn Ser Leu Gly Lys Thr Tyr Ala Lys Gly
1 5 10

<210> 33

<211> 12

<212> PRT

<213> Neuronal nicotinic acetylcholine receptor alpha 3 subunit
(CHRNA3) [Swiss-Prot: Q8VHH6/P04757/Q8R4G9/P32297]: FGFR binding motif

<400> 33

Ile Ala Glu Asn Met Lys Ala Gln Asn Glu Ala Lys
1 5 10

<210> 34

<211> 16

<212> PRT

<213> Neuronal acetylcholine receptor protein, alpha-6 chain precursor (CHRNA6) [Swiss-prot:]: FGFR binding motif

<400> 34

Gln Phe Ile Ala Glu Asn Met Lys Ser His Asn Glu Thr Lys Glu Val
1 5 10 15

<210> 35

<211> 13

<212> PRT

<213> ROBO-1 [O44924]: FGFR binding motif

<400> 35

Gly Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln
1 5 10

<210> 36

<211> 13

<212> PRT

<213> ROBO-1[AF041082; Q9Y6N7]: FGFR binding motif

<400> 36

Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val Gly Lys
1 5 10

<210> 37

<211> 14

<212> PRT

<213> ROBO-1[AF041082; Q9Y6N7]: FGFR binding motif

<400> 37

Gly Lys Tyr Val Cys Val Gly Thr Asn Met Val Gly Glu Arg
1 5 10

<210> 38

<211> 11

<212> PRT

<213> FGFR2 [Q96KM2; P21802]: FGFR binding motif

<400> 38

Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly
1 5 10

<210> 39

<211> 12

<212> PRT

<213> FGFR2[Q63241]: FGFR binding site

<400> 39

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly
1 5 10

<210> 40

<211> 11

<212> PRT

<213> Fc receptor-like protein 1[Q96KM2] / fragment of IFGP 1
[Q96PJ6]: FGFR binding motif

<400> 40

Gln Tyr Tyr Cys Val Ala Glu Asn Gly Tyr Gly
1 5 10

<210> 41

<211> 13

<212> PRT

<213> Junctional adhesion molecule (JAM-1) [Q9JKD5/O88792]: FGFR
binding motif

<400> 41

Gly Glu Tyr Tyr Gln Glu Ala Glu Gln Asn Gly Tyr Gly
1 5 10

<210> 42

<211> 12

<212> PRT

<213> FGFR1 [Q9QZM7/Q99QVV7; Q9UD50]: FGFR binding motif

<400> 42

Gly Asn Tyr Thr Cys Leu Val Glu Asn Glu Tyr Gly
1 5 10

<210> 43

<211> 12

<212> PRT

<213> Contactin precursor (Neural adhesion molecule
F3) [Q63198; P1260; Q12860]: FGFR binding motif

<400> 43

Gly Met Tyr Gln Cys Leu Ala Glu Asn Ala Tyr Gly
1 5 10

<210> 44

<211> 11

<212> PRT

<213> Contactin precursor (Neural adhesion molecule F3/F11)
[Q28106]: FGFR binding motif

<400> 44

Gly Met Tyr Gln Cys Ala Glu Asn Thr His Gly
1 5 10

<210> 45

<211> 12

<212> PRT

<213> Contactin precursor (Neural adhesion molecule F3/F11)
[Q28106]: FGFR binding motif

<400> 45

Gly Ile Tyr Tyr Cys Leu Ala Ser Asn Asn Tyr Gly
1 5 10

<210> 46

<211> 12

<212> PRT

<213> IFGP2[Q96PJ5]: FGFR binding motif

<400> 46

Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Ser Tyr Gly
15

<211> 12

<212> PRT

<213> Neurofascin 155 Da isoform [Q91Z60]: FGFR binding motif

<400> 50

Gly Glu Tyr Phe Cys Leu Ala Ser Asn Lys Met Gly
1 5 10

<210> 51

<211> 12

<212> PRT

<213> Macrophage scavenger receptor 2 (MSR2) [Q91YK7]:FGFR
binding motif

<400> 51

Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Asn Tyr Gly
1 5 10

<210> 52

<211> 14

<212> PRT

<213> Macrophage scavenger receptor 2 (MSR2) [Q91YK7]: FGFR
binding motif

<400> 52

Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ala Trp Gly Thr Lys
1 5 10

<210> 53

<211> 12

<212> PRT

<213> Neural cell adhesion molecule L1[Q9QYQ7; Q9QY38; P11627; Q05695; P32004]: FGFR binding motif

<400> 53

Gly Glu Tyr Thr Cys Leu Ala Glu Asn Ser Leu Gly
1 5 10

<210> 54

<211> 13

<212> PRT

<213> Neural-glial cell adhesion molecule Ng-CAM [Q03696]: FGFR binding motif

<400> 54

Gly Glu Tyr Glu Cys Val Ala Glu Asn Gly Arg Leu Gly
1 5 10

<210> 55

<211> 13

<212> PRT

<213> FGFR3 [Q95M13; AF487554; Q99052]: FGFR binding motif

<400> 55

Gly Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Arg
1 5 10

<210> 56

<211> 12

<212> PRT

<213> FGFR3 [Q95M13; Q99052]: FGFR binding motif

<400> 56

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly
1 5 10

<210> 57

<211> 12

<212> PRT

<213> Neural cell adhesion molecule 2 (NCAM2) [P36335]: FGFR
binding motif

<400> 57

Gly Glu Tyr Phe Cys Val Ala Ser Asn Pro Ile Gly
1 5 10

<210> 58

<211> 12

<212> PRT

<213> Neural cell adhesion molecule 2 (NCAM2) [P36335]: FGFR
binding motif

<400> 58

Glu Tyr Thr Cys Ile Ala Asn Asn Gln Ala Gly Glu
1 5 10

<210> 59

<211> 13

<212> PRT

<213> Axonin-1 (TAG-1) [Q02246;P22063; P28685]: FGFR binding
motif

<400> 59

Gly Met Tyr Gln Cys Val Ala Glu Asn Lys His Leu Gly
1 5 10

<210> 60

<211> 13

<212> PRT

<213> Neural cell adhesion molecule NCAM-140 AND ncam-140
[P13595]: FGFR binding motif

<400> 60

Gly Glu Tyr Met Cys Thr Ala Ser Asn Thr Ile Gly Gln
1 5 10

<210> 61

<211> 13

<212> PRT

<213> Neural cell adhesion molecule NCAM-140 AND ncam-140
[P13595]: FGFR binding motif

<400> 61

Glu Tyr Val Cys Ile Ala Glu Asn Lys Ala Gly Glu Gln
1 5 10

<210> 62

<211> 13

<212> PRT

<213> Neurotrophin receptor tyrosin kinase type 2 (NTRKT)
[Q8WXJ5]: FGFR binding motif

<400> 62

Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly Lys
1 5 10

<210> 63

<211> 12

<212> PRT

<213> Colorectal cancer suppressor DCC [P43146]: FGFR binding motif

<400> 63

Gly Phe Tyr Gln Cys Val Ala Glu Asn Glu Ala Gly
1 5 10

<210> 64

<211> 14

<212> PRT

<213> Tyrosine phosphatase LAR (ptprf) [Q9EQ17; Q64604; P23468]: FGFR binding motif

<400> 64

Gly Lys Tyr Glu Cys Val Ala Thr Asn Ser Ala Gly Thr Arg
1 5 10

<210> 65

<211> 12

<212> PRT

<213> Platelet-derived growth factor receptor beta (PDGFRB) [Q8R406; Q05030]: FGFR binding motif

<400> 65

Gly Glu Tyr Phe Cys Val Tyr Asn Asn Ser Leu Gly
1 5 10

<210> 66

<211> 13

<212> PRT

<213> Intercellular adhesion molecule-5 (ICAM-5, telencephalin)
[Q8TAM9; Q60625]: FGFR binding motif

<400> 66

Gly	Glu	Tyr	Glu	Cys	Ala	Ala	Thr	Asn	Ala	His	Gly	Arg
1				5					10			

<210> 67

<211> 13

<212> PRT

<213> B-cell receptor CD22 precursor (Leu-14; B-lymphocyte cell
adhesion molecule) [P20273]: FGFR binding motif

<400> 67

Gly	Ala	Tyr	Trp	Cys	Gln	Gly	Thr	Asn	Ser	Val	Gly	Lys
1				5					10			

<210> 68

<211> 12

<212> PRT

<213> B-cell receptor CD22 precursor (Leu-14; B-lymphocyte cell
adhesion molecule) [P20273]: FGFR binding motif

<400> 68

Gly	Thr	Tyr	Ser	Cys	Val	Ala	Glu	Asn	Ile	Leu	Gly
1				5					10		

<210> 69

<211> 14

<212> PRT

<213> NCAM-2 [Swiss-Prot: O15394; O35136]: FGFR binding motif

<400> 69

Arg Val Ala Ala Val Asn Gly Lys Gly Gln Gly Asp Tyr Ser
1 5 10

<210> 70

<211> 14

<212> PRT

<213> HCF-2 (Host cell factor 2) [Swiss-Prot: Q9Y5Z7]: FGFR
binding motif: FGFR binding motif

<400> 70

Arg Val Ala Ala Ile Asn Gly Cys Gly Ile Gly Pro Phe Ser
1 5 10

<210> 71

<211> 9

<212> PRT

<213> ICLN (Chloride channel regulator, inducer) [Swiss-Prot:
P97506; Q9NRD2; Q61189; P54105]: FGFR binding motif

<400> 71

Ala Val Leu Asn Gly Lys Gly Leu Gly
1 5

<210> 72

<211> 11

<212> PRT

<213> Galectin-12 [Swiss-Prot: Q91VD1; Q9JKX2; Q9NZ03]: FGFR
binding motif

<400> 72

Ala Leu Asn Gly Gln Gly Leu Gly Ala Thr Ser
1 5 10

<210> 73

<211> 12

<212> PRT

<213> Human receptor-like protein tyrosine phosphatase leukocyte
common antigen-related molecule (PTPRF) [Swiss-Prot: P10586]: FGFR
binding motif

<400> 73

Arg Leu Ala Ala Lys Asn Arg Ala Gly Leu Gly Glu
1 5 10

<210> 74

<211> 13

<212> PRT

<213> Natural resistance-associated macrophage protein 1 (NRAMP-1,
SLC11A1) [Swiss-Prot: O77741]: FGFR binding motif

<400> 74

Arg Leu Gly Val Val Thr Gly Lys Asp Leu Gly Glu Ile
1 5 10

<210> 75

<211> 14

<212> PRT

<213> NCAM2 (180 kDa isoform precursor) [Swiss-Prot: P36335]:
FGFR binding motif

<400> 75

Thr Val Thr Gly Leu Lys Pro Glu Thr Ser Tyr Met Val Lys
1 5 10

<210> 76

<211> 13

<212> PRT

<213> Nephrin [Swiss-Prot: Q925S5; Q9JIX2; Q9ET59; Q9R044;
Q9QZS7]: FGFR binding motif

<400> 76

Thr Leu Thr Gly Leu Lys Pro Ser Thr Arg Tyr Arg Ile
1 5 10

<210> 77

<211> 13

<212> PRT

<213> Nephrin [Swiss-Prot: O60500]: FGFR binding motif

<400> 77

Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg Tyr Arg Val
1 5 10

<210> 78

<211> 14

<212> PRT

<213> Tyrosine phosphatase LAR (PTPRF) [Swiss-Prot : Q9EQ17]:

FGFR binding motif

<400> 78

Thr Leu Leu Gly Leu Lys Pro Asp Thr Thr Tyr Asp Ile Lys
1 5 10

<210> 79

<211> 14

<212> PRT

<213> Leukocyte common antigen-related phosphatase ptp2 precursor
(LAR-PTP2) [Swiss-Prot: Q64605]: FGFR binding motif

<400> 79

Thr Leu Gln Gly Leu Arg Pro Glu Thr Ala Tyr Glu Leu Arg
1 5 10

<210> 80

<211> 14

<212> PRT

<213> Protein-tyrosine phosphatase, receptor-type, S precursor
(EC 3.1.3.48) (Protein-tyrosine phosphatase sigma) (RPTP-sigma)
[Swiss-Prot: Q64699]: FGFR binding motif

<400> 80

Thr Leu Arg Gly Leu Arg Pro Glu Thr Ala Tyr Glu Leu Arg
1 5 10

<210> 81

<211> 14

<212> PRT

<213> Tyrosine-protein kinase receptor Tie-1 precursor (TIE1.)
(EC 2.7.1.112) [Swiss-Prot: Q06805; P35590]: FGFR binding motif

<400> 81

Thr Leu Met Asn Leu Arg Pro Lys Thr Gly Tyr Ser Val Arg
1 5 10

<210> 82

<211> 11

<212> PRT

<213> Ephrin type-A receptor 8 precursor to (EPHA8..) (EC 2.7.1.112) (Tyrosine-protein kinase receptor EEK) (EPH-and ELK-related kinase)]: FGFR binding motif

<400> 82

Thr Val Ser Gly Leu Lys Pro Gly Thr Arg Tyr
1 5 10

<210> 83

<211> 11

<212> PRT

<213> Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (CEK4) (EPHA3..) [tn: P29318]: FGFR binding motif

<400> 83

Thr Ile Ser Gly Leu Lys Pro Asp Thr Thr Tyr
1 5 10

<210> 84

<211> 11

<212> PRT

<213> Protein-tyrosine phosphatase receptor-type S precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase sigma, PTPRS) [Swiss-Prot:

Q13332]: FGFR binding motif

<400> 84

Thr Leu Gln Gly Leu Lys Pro Asp Thr Ala Tyr
1 5 10

<210> 85

<211> 12

<212> PRT

<213> Insulin receptor [Swiss-Prot: Q9PWN6]: FGFR binding motif

<400> 85

Leu Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Val
1 5 10

<210> 86

<211> 13

<212> PRT

<213> Type VII collagen [Swiss-Prot: Q63870]: FGFR binding motif

<400> 86

Ile Asp Gly Leu Glu Pro Asp Thr Glu Tyr Ile Val Arg
1 5 10

<210> 87

<211> 12

<212> PRT

<213> Insulin-like growth factor-1 receptor precursor
[Swiss-Prot: O73798]: FGFR binding motif

<400> 87

Leu Gln Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile
1 5 10

<210> 88

<211> 14

<212> PRT

<213> Fibronectin [Swiss-Prot: Q95KV4; Q95KV5; P07589; Q28377;
U42594; O95609]: FGFR binding motif

<400> 88

Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Gln
1 5 10

<210> 89

<211> 10

<212> PRT

<213> Insulin-like growth factor I receptor (IGF I receptor
beta-subunit, IGF I receptor alpha-subunit) [Swiss-Prot: Q9QVW4;
P08069; P24062; Q60751; P15127; P15208]: FGFR binding motif

<400> 89

Gly Leu Lys Pro Trp Thr Gln Tyr Ala Val
1 5 10

<210> 90

<211> 13

<212> PRT

<213> Insulin receptor-related protein precursor (EC 2.7.1.112)
(IRR) (IR-related receptor) [Swiss-Prot: P14616]: FGFR binding
motif

<400> 90

Thr Leu Ala Ser Leu Lys Pro Trp Thr Gln Tyr Ala Val
1 5 10

<210> 91

<211> 12

<212> PRT

<213> Tenascin-R (restrictin) [Swiss-Prot: Q15568; O00531]: FGFR binding motif

<400> 91

Leu Met Gly Leu Gln Pro Ala Thr Glu Tyr Ile Val
1 5 10

<210> 92

<211> 14

<212> PRT

<213> Neogenin precursor (NEO1..) [Swiss-Prot: Q92859; P97603; Q90610; P97798]: FGFR binding motif

<400> 92

Lys Gly Met Gly Pro Met Ser Glu Ala Val Gln Phe Arg Thr
1 5 10

<210> 93

<211> 14

<212> PRT

<213> Protein tyrosine phosphatase receptor type D (PTPRD, BA175E13.1) [Swiss-Prot: Q8WX65; Q9IAJ1; P23468; Q64487]: FGFR binding motif

<400> 93

Thr Leu Thr Gly Leu Lys Pro Asp Thr Thr Tyr Asp Val Lys
 1 5 10

<210> 94

<211> 12

<212> PRT

<213> Protein tyrosine phosphatase receptor type D (PTPRD, BA175E13.1) [Swiss-Prot: Q8WX65; Q9IAJ1; P23468; Q64487]: FGFR binding motif

<400> 94

Ile Ser Gly Leu Gln Pro Glu Thr Ser Tyr Ser Leu
 1 5 10

<210> 95

<211> 14

<212> PRT

<213> Protein-tyrosine phosphatase receptor-type F precursor (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) [Swiss-Prot: Q64604; Q9QW67; P10586]: FGFR binding motif

<400> 95

Thr Leu Leu Gly Leu Lys Pro Asp Thr Thr Tyr Asp Ile Lys
 1 5 10

<210> 96

<211> 13

<212> PRT

<213> Protein-tyrosine phosphatase receptor-type F precursor (EC 3.1.3.48) (Leukocyte antigen related) [Swiss-Prot: Q64604; Q9QW67; P10586]: FGFR binding motif

<400> 96

Thr Ile Ser Gly Leu Thr Pro Glu Thr Thr Tyr Ser Ile
1 5 10

<210> 97

<211> 13

<212> PRT

<213> CD22 [Q9R094]: FGFR binding motif

<400> 97

Gly Asn Tyr Ser Cys Leu Ala Glu Asn Arg Leu Gly Arg
1 5 10

<210> 98

<211> 12

<212> PRT

<213> FGFR-4 [Q91742]: FGFR binding motif

<400> 98

Gly Asn Tyr Thr Cys Val Val Glu Asn Arg Val Gly
1 5 10

<210> 99

<211> 12

<212> PRT

<213> ICAM-5 [Q8TAM9]: FGFR binding motif

<400> 99

Gly Thr Tyr His Cys Val Ala Thr Asn Ala His Gly
1 5 10

<210> 100

<211> 14

<212> PRT

<213> FIII,4 domain of L1: FGFR binding motif [Swiss-Prot:
Q9QY38]

<400> 100

Leu Ser His Asn Gly Val Leu Thr Gly Tyr Leu Leu Ser Tyr
1 5 10

<210> 101

<211> 11

<212> PRT

<213> Neuron-glia cell adhesion molecule (Ng-CaM) precursor
.[Gallus gallus]; [Swiss-Prot: Q90933]: FGFR binding motif

<400> 101

Asn Gly Val Leu Thr Gly Tyr Val Leu Arg Tyr
1 5 10

<210> 102

<211> 11

<212> PRT

<213> Neurofascin precursor .[Gallus gallus]; [Swiss-Prot:
O42414]: FGFR binding motif

<400> 102

Asn Gly Val Leu Thr Gly Tyr Asn Leu Arg Tyr
1 5 10

<210> 103

<211> 11

<212> PRT

<213> (CALL) Neural cell adhesion molecule. [Homo sapiens] .[
Swiss-Prot: O00533]: FGFR binding motif

<400> 103

Asn Gly Asn Leu Thr Gly Tyr Leu Leu Gln Tyr
1 5 10

<210> 104

<211> 14

<212> PRT

<213> f Neuroglial.[Manduca sexta] .[Swiss-Prot: P91767]: FGFR
binding motif

<400> 104

Val Asp Glu Asn Gly Val Leu Thr Gly Tyr Lys Ile Tyr Tyr
1 5 10

<210> 105

<211> 13

<212> PRT

<213> Protein-tyrosine phosphatase sigma [Swiss-Prot: O75870];
and [Swiss-Prot: Q13332] [Homo sapiens] :FGFR binding motif

<400> 105

Thr His Asn Gly Ala Leu Val Gly Tyr Ser Val Arg Tyr
1 5 10

<210> 106

<211> 11

<212> PRT

<213> NR-CaM 12 [Rattus sp] , [Swiss-Prot: Q9QVN3]: FGFR binding motif

<400> 106

Asn Gly Ile Leu Thr Glu Tyr Ile Leu Lys Tyr
1 5 10

<210> 107

<211> 11

<212> PRT

<213> Neurofascin 155 kDa isoform.[Rattus norvegicus],[
Swiss-Prot: Q91Z60]: FGFR binding motif

<400> 107

Asn Gly Ile Leu Ile Gly Tyr Thr Leu Arg Tyr
1 5 10

<210> 108

<211> 13

<212> PRT

<213> Neogenin (Fragment).[Gallus gallus], [Swiss-Prot: Q90610]:
FGFR binding motif

<400> 108

Thr His Ser Gly Gln Ile Thr Gly Tyr Lys Ile Arg Tyr
1 5 10

<210> 109

<211> 11

<212> PRT

<213> Neogenin (Fragment).[Gallus gallus], [Swiss-Prot: Q90610]:FGFR binding motif

<400> 109

Asn Gly Lys Ile Thr Gly Tyr Ile Ile Tyr Tyr
1 5 10

<210> 110

<211> 10

<212> PRT

<213> Metalloprotease 1 (pitrilysin family).[Homo sapiens] [Swiss-Prot: Q9BSI6]:FGFR binding motif

<400> 110

Leu Ser His Asn Gly Ile Phe Thr Leu Tyr
1 5 10

<210> 111

<211> 11

<212> PRT

<213> HBRAVO/Nr-CaM.[Homo sapiens].[Swiss-Prot: Q92823; O15179]:FGFR binding motif

<400> 111

Asn Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr
1 5 10

<210> 112

<211> 14

<212> PRT

<213> Protein-tyrosine phosphatase kappa precursor (EC 3.1.3.48)

(R-PTP-kappa).[Homo sapiens].[Swiss-Prot: Q15262]: FGFR binding motif

<400> 112

Leu Asp Pro Asn Gly Ile Ile Thr Gln Tyr Glu Ile Ser Tyr
1 5 10

<210> 113

<211> 11

<212> PRT

<213> Neogenin precursor (NEO1..).[Homo sapiens and Mus musculus][Swiss-Prot: Q92859; P97798]: FGFR binding motif

<400> 113

Asn Gly Lys Ile Thr Gly Tyr Ile Ile Tyr Tyr
1 5 10

<210> 114

<211> 15

<212> PRT

<213> Neural cell adhesion L1(SPLICE ISOFORM 2) [Homo sapiens [Swiss-Prot: P32004]; [Mus musculus Swiss-Prot: Q9QY38]: FGFR binding motif

<400> 114

His Leu Glu Val Gln Ala Phe Asn Gly Arg Gly Ser Gly Pro Ala
1 5 10 15

<210> 115

<211> 14

<212> PRT

<213> NB-2.[Rattus norvegicus] [Swiss-Prot: P97527]:FGFR binding

motif

<400> 115

His Leu Thr Val Arg Ala Tyr Asn Gly Ala Gly Tyr Gly Pro
1 5 10

<210> 116

<211> 15

<212> PRT

<213> Neural cell adhesion protein BIG-2 precursor. [Rattus norvegicus] [Swiss-Prot: Q62845]: FGFR binding motif

<400> 116

His Leu Ser Val Lys Ala Tyr Asn Ser Ala Gly Thr Gly Pro Ser
1 5 10 15

<210> 117

<211> 15

<212> PRT

<213> Axonal-associated cell adhesion molecule. [Homo sapiens]. [Swiss-Prot: Q8TC35]: FGFR binding motif

<400> 117

His Leu Ala Val Lys Ala Tyr Asn Ser Ala Gly Thr Gly Pro Ser
1 5 10 15

<210> 118

<211> 14

<212> PRT

<213> Contactin A/F3/F11. [Xenopus laevis] [Swiss-Prot: O93250]: FGFR binding motif

<400> 118

Asn Leu Glu Val Arg Ala Phe Asn Ser Ala Gly Asp Gly Pro
1 5 10

<210> 119

<211> 14

<212> PRT

<213> Neural cell adhesion molecule CALL.[Homo sapiens][Swiss-Prot: O00533]:FGFR binding motif

<400> 119

His Leu Thr Val Leu Ala Tyr Asn Ser Lys Gly Ala Gly Pro
1 5 10

<210> 120

<211> 13

<212> PRT

<213> Neuron-glia cell adhesion molecule (Ng-CaM) precursor.[Gallus gallus][Swiss-Prot: Q909339]: FGFR binding motif

<400> 120

Leu Arg Val Leu Val Phe Asn Gly Arg Gly Asp Gly Pro
1 5 10

<210> 121

<211> 14

<212> PRT

<213> Contactin precursor (Neural cell recognition molecule F11).[Gallus gallus][Swiss-Prot: P14781]: FGFR binding motif

<400> 121

His Ile Asp Val Ser Ala Phe Asn Ser Ala Gly Tyr Gly Pro
1 5 10

<210> 122

<211> 10

<212> PRT

<213> SLIT [Drosophila melanogaster][Swiss-Prot: Q9XYV4]: FGFR
binding motif

<400> 122

His Leu Ala Val Glu Leu Phe Asn Gly Arg
1 5 10

<210> 123

<211> 14

<212> PRT

<213> Galectin-4.[Mus musculus][Swiss-Prot: Q8K419, P38552]:
FGFR binding motif

<400> 123

Leu Glu Leu Gln Ser Ile Asn Phe Leu Gly Gly Gln Pro Ala
1 5 10

<210> 124

<211> 14

<212> PRT

<213> HNB-2.[Homo sapiens]Swiss-Prot: O94779: FGFR binding motif

<400> 124

His Phe Thr Val Arg Ala Tyr Asn Gly Ala Gly Tyr Gly Pro
1 5 10

<210> 125

<211> 15

<212> PRT

<213> The EFL peptide (from the FIII,3 domain of L1) [Swiss-Prot:
P32004]: FGFR binding motif

<400> 125

His Leu Glu Val Gln Ala Phe Asn Gly Arg Gly Ser Gln Pro Ala
1 5 10 15

<210> 126

<211> 14

<212> PRT

<213> Fragment of Neuroglial (Drosophila) [Swiss-prot: P202419]:
FGFR binding motif

<400> 126

Val Ile Ala Asp Gln Pro Thr Phe Val Lys Tyr Leu Ile Lys
1 5 10

<210> 127

<211> 14

<212> PRT

<213> Fragment of Fibronectin (bovine) [Swiss-prot: P07589]: FGFR
binding motif

<400> 127

Thr Ile Lys Gly Leu Arg Pro Gly Val Val Tyr Glu Gly Gln
1 5 10

<210> 128

<211> 14

<212> PRT

<213> Tenascin (chick) [Swiss-prot: P10039]: FGFR binding motif

<400> 128

Thr Leu Thr Glu Leu Ser Pro Ser Thr Gln Tyr Thr Val Lys
1 5 10

<210> 129

<211> 14

<212> PRT

<213> Ephrin type A receptor2 [Swiss-prot: Q8N3Z2]: FGFR binding motif

<400> 129

Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln
1 5 10

<210> 130

<211> 14

<212> PRT

<213> LAR [Swiss-prot Q9VIS8]: FGFR binding motif

<400> 130

Thr Val Ser Asp Val Thr Pro His Ala Ile Tyr Thr Val Arg
1 5 10

<210> 131

<211> 14

<212> PRT

<213> RTK (Tie-1,hu) [Swiss-prot P35590]: FGFR binding motif

<400> 131

Ile Ile Arg Gly Leu Asn Ala Ser Thr Arg Tyr Leu Phe Arg
1 5 10

<210> 132

<211> 14

<212> PRT

<213> RTK (Tie-1,hu) [Swiss-prot P35590]: FGFR binding motif

<400> 132

Thr Leu Met Asn Leu Arg Pro Lys Thr Gly Tyr Ser Val Arg
1 5 10

<210> 133

<211> 14

<212> PRT

<213> Consensus sequence (conserved domain database) : FGFR
binding motif

<400> 133

Thr Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Glu Val Arg
1 5 10

<210> 134

<211> 14

<212> PRT

<213> The beta-common cytokine receptor of IL-3, IL-5 and GmCsf
[Swiss-prot P32927]: FGFR binding motif

<400> 134

Gly Pro Glu His Leu Met Pro Ser Ser Thr Tyr Val Ala Arg
1 5 10

<210> 135

<211> 14

<212> PRT

<213> Unc-22 (C. Elegance). [Swiss-prot: Q23550]: FGFR binding
motif

<400> 135

Arg Val Thr Gly Leu Thr Pro Lys Lys Thr Tyr Glu Phe Arg
1 5 10

<210> 136

<211> 14

<212> PRT

<213> Consensus sequence (conserved domain database): FGFR
binding motif

<400> 136

Thr Leu Thr Gly Leu Lys Pro Gly Thr Glu Tyr Glu Phe Arg
1 5 10

<210> 137

<211> 15

<212> PRT

<213> Consensus sequence (conserved domain database): FGFR
binding motif

<400> 137

Glu Val Arg Val Gln Ala Val Asn Gly Gly Gly Asn Gly Pro Pro
1 5 10 15

<210> 138

<211> 12

<212> PRT

<213> Drosophila Neuroglial [Swiss-prot: P20241]: FGFR binding
motif

<400> 138

Leu Ile Lys Val Val Ala Ile Asn Asp Arg Gly Glu
1 5 10

<210> 139

<211> 12

<212> PRT

<213> Fibronectin (mouse) [Swiss-prot: P11276]: FGFR binding
motif

<400> 139

Val Val Ser Ile Ile Ala Val Asn Gly Arg Glu Glu
1 5 10

<210> 140

<211> 12

<212> PRT

<213> Fibronectin (bovine) [Swiss-prot: P07589]: FGFR binding
motif

<400> 140

Val Val Ser Val Tyr Ala Gln Asn Gln Asn Gly Glu
1 5 10

<210> 141

<211> 12

<212> PRT

<213> Tenascin (chick) [Swiss-prot: Q90995]: FGFR binding motif

<400> 141

Thr Ile Ser Leu Val Ala Glu Lys Gly Arg His Lys
1 5 10

<210> 142

<211> 15

<212> PRT

<213> L1 (human, F3,EFL) [Swiss-prot: P32004]: FGFR binding motif

<400> 142

His Leu Glu Val Gln Ala Phe Asn Gly Arg Gly Ser Gly Pro Ala
1 5 10 15

<210> 143

<211> 15

<212> PRT

<213> L1 (mouse, F3,EFL) [Swiss-prot: P11627]: FGFR binding motif

<400> 143

His Val Glu Val Gln Ala Phe Asn Gly Arg Gly Leu Gly Pro Ala
1 5 10 15

<210> 144

<211> 15

<212> PRT

<213> L1 (rat, F3,EFL) [Swiss-prot: Q05695]: FGFR binding motif

<400> 144

His Val Glu Val Gln Ala Phe Asn Gly Arg Gly Leu Gly Pro Ala
1 5 10 15

<210> 145

<211> 13

<212> PRT

<213> Consensus sequence (conserved domain database): FGFR
binding motif

<400> 145

Glu Phe Arg Val Arg Ala Val Asn Gly Ala Gly Glu Gly
1 5 10

<210> 146

<211> 15

<212> PRT

<213> The beta-common cytokine receptor of IL-3. IL-5 and GmCsf
[Swiss-prot: P32927]: FGFR binding motif

<400> 146

Val Ala Arg Val Arg Thr Arg Leu Ala Pro Gly Ser Arg Leu Ser
1 5 10 15